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SEQUENCE LISTING

TECH CENTER 1600/2900

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Cole, Douglas G.

<120> INTRAFLAGELLAR TRANSPORT

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<140> US 09/866,582

<141> 2001-05-24

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<151> 2000-05-24

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Met
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gac gcg gta gat aga gga gtc tac ttt gac gag gac ttt cat gtc cgc 164
Asp Ala Val Asp Arg Gly Val Tyr Phe Asp Glu Asp Phe His Val Arg
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Ile Leu Asp Val Asp Lys Tyr Asn Ala Ser Lys Ser Leu Gln Asp Asn
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aca aat gtg ttc att aac aac atc caa aat atg caa ggc ctc gtg gac 260
Thr Asn Val Phe Ile Asn Asn Ile Gln Asn Met Gln Gly Leu Val Asp
35 40 45

aag tac gtg tcc gcc atc gac cag cag gtc gag cgg cta gaa gct gaa 308
Lys Tyr Val Ser Ala Ile Asp Gln Gln Val Glu Arg Leu Glu Ala Glu
50 55 60 65

aag ctg aag gcc att ggc ctg cgg aac cgg gtg gct gcg ctg agc gag 356
Lys Leu Lys Ala Ile Gly Leu Arg Asn Arg Val Ala Ala Leu Ser Glu
70 75 80

gag	cgg	aaa	cgt	aaa	caa	aag	gag	cag	gag	cgc	atg	cta	gct	gag	aag		404
Glu	Arg	Lys	Arg	Lys	Gln	Lys	Glu	Gln	Glu	Arg	Met	Leu	Ala	Glu	Lys		
85							90					95					
cag	gag	gag	ctt	gag	agg	ctc	caa	atg	gag	gag	cag	tcg	ctg	atc	aag		452
Gln	Glu	Glu	Leu	Glu	Arg	Leu	Gln	Met	Glu	Glu	Gln	Ser	Leu	Ile	Lys		
100							105					110					
gtg	aag	ggc	gag	cag	gag	ctc	atg	att	cag	aag	ctg	tcg	gac	agc	agc		500
Val	Lys	Gly	Glu	Gln	Glu	Leu	Met	Ile	Gln	Lys	Leu	Ser	Asp	Ser	Ser		
115							120				125						
agc	ggg	gct	gca	tac	gtg	taaacgggt	tccggacgtca	tgcgtgcaaa								548	
Ser	Gly	Ala	Ala	Tyr	Val												
130							135										
ggtagttgc	tctgtgaggg	ttggctgagg	cggcgaggc	tgctattgag	gctgcagcat											608	
gcgtctgg	ggcagatgt	cataacggta	tgggtgtt	gacacaac	gaaacggcga											668	
gggtgcgca	atgtcgtgca	gaagcgacgc	tacagcatcc	atggtacgta	gaggcttact											728	
gggtgtcagt	gcgtcgccg	ccactgggg	cacacttgca	gcgaggagcg	ccattgttt											788	
gcccacggat	tgcgtcaagg	acttgaacgg	cgccagtgaa	ggcgggaaat	ggaatgtaaa											848	
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Asn	Thr	Asn	Val	Phe	Ile	Asn	Asn	Ile	Gln	Asn	Met	Gln	Gly	Leu	Val		
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Asp	Lys	Tyr	Val	Ser	Ala	Ile	Asp	Gln	Gln	Val	Glu	Arg	Leu	Glu	Ala		
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Glu	Lys	Leu	Lys	Ala	Ile	Gly	Leu	Arg	Asn	Arg	Val	Ala	Ala	Leu	Ser		
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Glu	Glu	Arg	Lys	Gln	Lys	Glu	Gln	Glu	Gln	Glu	Arg	Met	Leu	Ala	Glu		
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Lys	Gln	Glu	Glu	Leu	Glu	Arg	Leu	Gln	Met	Glu	Glu	Gln	Ser	Leu	Ile		
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Lys	Val	Lys	Gly	Glu	Gln	Glu	Leu	Met	Ile	Gln	Lys	Leu	Ser	Asp	Ser		
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Cys Lys Val Ala Val Val Gly Glu Ala Thr Val Gly Lys Ser Ala Leu
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Ile Ser Met Phe Thr Ser Lys Gly Ser Lys Phe Leu Lys Asp Tyr Ala
35 40 45

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Met Thr Ser Gly Val Glu Val Val Ala Pro Val Thr Ile Pro Asp
50 55 60

acg acg gtc tcg gtg gag ctc ttt ctg ctg gac acg gcg ggg agc gac 240
Thr Thr Val Ser Val Glu Leu Phe Leu Leu Asp Thr Ala Gly Ser Asp
65 70 75 80

ctg tac aag gag cag ata tcg cag tac tgg aac ggc gta tac tac gcc 288
Leu Tyr Lys Glu Gln Ile Ser Gln Tyr Trp Asn Gly Val Tyr Tyr Ala
85 90 95

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Ile Leu Val Phe Asp Val Ser Ser Met Glu Ser Phe Glu Ser Cys Lys
100 105 110

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Ala Trp Phe Glu Leu Leu Lys Ser Ala Arg Pro Asp Arg Glu Arg Pro
115 120 125

ctg cgc gcc gtg ctg gtg gcg aac aag acg gac ctt ccg ccg cag cgg 432
Leu Arg Ala Val Leu Val Ala Asn Lys Thr Asp Leu Pro Pro Gln Arg
130 135 140

cac cag gtg cgg ctg gac atg gcg cag gac tgg gcc acc acc aac acc 480
His Gln Val Arg Leu Asp Met Ala Gln Asp Trp Ala Thr Thr Asn Thr
145 150 155 160

ctc gac ttc ttc gac gtg tcc gcg aac ccg ccc ggc aag gac gcg gat 528
Leu Asp Phe Phe Asp Val Ser Ala Asn Pro Pro Gly Lys Asp Ala Asp
165 170 175

gcg ccg ttc ctg tcc atc gcc acc acc ttc tac cgc aac tac gag gac 576
Ala Pro Phe Leu Ser Ile Ala Thr Thr Phe Tyr Arg Asn Tyr Glu Asp
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aag gtg gcg gcc ttc cag gac gct tgc cgc aac tac tga 615
Lys Val Ala Ala Phe Gln Asp Ala Cys Arg Asn Tyr
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<212> PRT
<213> Chlamydomonas reinhardtii

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 Ile Ser Met Phe Thr Ser Lys Gly Ser Lys Phe Leu Lys Asp Tyr Ala
 35 40 45
 Met Thr Ser Gly Val Glu Val Val Val Ala Pro Val Thr Ile Pro Asp
 50 55 60
 Thr Thr Val Ser Val Glu Leu Phe Leu Leu Asp Thr Ala Gly Ser Asp
 65 70 75 80
 Leu Tyr Lys Glu Gln Ile Ser Gln Tyr Trp Asn Gly Val Tyr Tyr Ala
 85 90 95
 Ile Leu Val Phe Asp Val Ser Ser Met Glu Ser Phe Glu Ser Cys Lys
 100 105 110
 Ala Trp Phe Glu Leu Leu Lys Ser Ala Arg Pro Asp Arg Glu Arg Pro
 115 120 125
 Leu Arg Ala Val Leu Val Ala Asn Lys Thr Asp Leu Pro Pro Gln Arg
 130 135 140
 His Gln Val Arg Leu Asp Met Ala Gln Asp Trp Ala Thr Thr Asn Thr
 145 150 155 160
 Leu Asp Phe Phe Asp Val Ser Ala Asn Pro Pro Gly Lys Asp Ala Asp
 165 170 175
 Ala Pro Phe Leu Ser Ile Ala Thr Thr Phe Tyr Arg Asn Tyr Glu Asp
 180 185 190
 Lys Val Ala Ala Phe Gln Asp Ala Cys Arg Asn Tyr
 195 200

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<213> Chlamydomonas reinhardtii

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cag ttc cag ggc acc gcg cgc tcg cag gtc gtg cag aac cag cag ccg cac	96
Gln Phe Gln Gly Thr Ala Arg Ser Gln Val Val Gln Asn Gln Pro His	
20 25 30	
gac gag gag gtg aac ctg agt gag tcg gag agc ttc gcg gga gcg gat	144
Asp Glu Glu Val Asn Leu Ser Glu Ser Glu Ser Phe Ala Gly Ala Asp	
35 40 45	
gag cct cca gct gcg cct aga gat gcg tcg ctc ata gag tca cac gac	192
Glu Pro Pro Ala Ala Pro Arg Asp Ala Ser Leu Ile Glu Ser His Asp	
50 55 60	

atg gac gag ggg cca gct gct cca gcg cgg aca ctc tca cca acg ggc Met Asp Glu Gly Pro Ala Ala Pro Ala Arg Thr Leu Ser Pro Thr Gly 65 70 75 80	240
tat gag gct gga aag cac gca cct ggc ggc atc gcc aac tcg gac gag Tyr Glu Ala Gly Lys His Ala Pro Gly Gly Ile Ala Asn Ser Asp Glu 85 90 95	288
gca ccg ccg ggt gct tac aac gca cag gag tac aag cac ctg aac gtg Ala Pro Pro Gly Ala Tyr Asn Ala Gln Glu Tyr Lys His Leu Asn Val 100 105 110	336
ggc gag gac gtg cgc gag ctg ttc tcc tac atc ggc cgc tac aag ccg Gly Glu Asp Val Arg Glu Leu Phe Ser Tyr Ile Gly Arg Tyr Lys Pro 115 120 125	384
cag acg gtg gag ctg gac acg cgc atc aag ccc ttc atc cct gac tac Gln Thr Val Glu Leu Asp Thr Arg Ile Lys Pro Phe Ile Pro Asp Tyr 130 135 140	432
atc ccc gcg gtg ggc atc gac gag ttc atc aag gtg ccg cga ccc Ile Pro Ala Val Gly Ile Asp Glu Phe Ile Lys Val Pro Arg Pro 145 150 155 160	480
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tcc aag gag gcg ccg ggc gcc aag gcc gac atg gtg ggg ccg ctg gag Ser Lys Glu Ala Pro Gly Ala Lys Ala Asp Met Val Gly Arg Leu Glu 195 200 205	624
cac acc gac gag aac aag gcc aag aag atc cag cag tgg atc gcc tcc His Thr Asp Glu Asn Lys Ala Lys Ile Gln Gln Trp Ile Ala Ser 210 215 220	672
atc aac gac atc cac aag gcc aag ccg gcc acc gtc aac tac agc Ile Asn Asp Ile His Lys Ala Lys Pro Ala Ala Thr Val Asn Tyr Ser 225 230 235 240	720
aag cgc atg cca gag atc gag gcg ctg atg cag gag tgg ccg ccg gag Lys Arg Met Pro Glu Ile Glu Ala Leu Met Gln Glu Trp Pro Pro Glu 245 250 255	768
gtg gag acc ttc ctc aag acc atg cac atg ccg tcc ggc gat gtg gag Val Glu Thr Phe Leu Lys Thr Met His Met Pro Ser Gly Asp Val Glu 260 265 270	816
ctg gac atc aag acc tac gcc ccg ctg gtg tgc acg ctg ctg gac att Leu Asp Ile Lys Thr Tyr Ala Arg Leu Val Cys Thr Leu Leu Asp Ile 275 280 285	864

ccc gtg tac gac gac ccc gtg gag agc ctg cac gtg ctg ttc aca ctg		912	
Pro Val Tyr Asp Asp Pro Val Glu Ser Leu His Val Leu Phe Thr Leu			
290	295	300	
tac ctg gag ttc aag aac aac ccc atc ttc agg cag cac atg gag atg		960	
Tyr Leu Glu Phe Lys Asn Asn Pro Ile Phe Arg Gln His Met Glu Met			
305	310	315	320
gag aac aag ctg gac ggc atg tcg ggc ggc ggc ggc atg atg ggc		1008	
Glu Asn Lys Leu Asp Gly Met Ser Gly Gly Gly Gly Met Met Gly			
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Gly Gly Ala Asp Val Leu Gly Leu			
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Asp Glu Glu Val Asn Leu Ser Glu Ser Glu Ser Phe Ala Gly Ala Asp			
35	40	45	
Glu Pro Pro Ala Ala Pro Arg Asp Ala Ser Leu Ile Glu Ser His Asp			
50	55	60	
Met Asp Glu Gly Pro Ala Ala Pro Ala Arg Thr Leu Ser Pro Thr Gly			
65	70	75	80
Tyr Glu Ala Gly Lys His Ala Pro Gly Gly Ile Ala Asn Ser Asp Glu			
85	90	95	
Ala Pro Pro Gly Ala Tyr Asn Ala Gln Glu Tyr Lys His Leu Asn Val			
100	105	110	
Gly Glu Asp Val Arg Glu Leu Phe Ser Tyr Ile Gly Arg Tyr Lys Pro			
115	120	125	
Gln Thr Val Glu Leu Asp Thr Arg Ile Lys Pro Phe Ile Pro Asp Tyr			
130	135	140	
Ile Pro Ala Val Gly Gly Ile Asp Glu Phe Ile Lys Val Pro Arg Pro			
145	150	155	160
Asp Thr Lys Pro Asp Tyr Leu Gly Leu Lys Val Leu Asp Glu Pro Ala			
165	170	175	
Ala Lys Gln Ser Asp Pro Thr Val Leu Thr Leu Gln Leu Arg Gln Leu			
180	185	190	
Ser Lys Glu Ala Pro Gly Ala Lys Ala Asp Met Val Gly Arg Leu Glu			
195	200	205	
His Thr Asp Glu Asn Lys Ala Lys Lys Ile Gln Gln Trp Ile Ala Ser			
210	215	220	
Ile Asn Asp Ile His Lys Ala Lys Pro Ala Ala Thr Val Asn Tyr Ser			
225	230	235	240
Lys Arg Met Pro Glu Ile Glu Ala Leu Met Gln Glu Trp Pro Pro Glu			
245	250	255	
Val Glu Thr Phe Leu Lys Thr Met His Met Pro Ser Gly Asp Val Glu			
260	265	270	

Leu Asp Ile Lys Thr Tyr Ala Arg Leu Val Cys Thr Leu Leu Asp Ile
 275 280 285
 Pro Val Tyr Asp Asp Pro Val Glu Ser Leu His Val Leu Phe Thr Leu
 290 295 300
 Tyr Leu Glu Phe Lys Asn Asn Pro Ile Phe Arg Gln His Met Glu Met
 305 310 315 320
 Glu Asn Lys Leu Asp Gly Met Ser Gly Gly Gly Gly Met Met Gly
 325 330 335
 Gly Gly Ala Asp Val Leu Gly Leu
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 <213> Chlamydomonas reinhardtii

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 Met Glu Glu Pro Gly Ala Glu
 1 5

gag gtt cgg att ctc ttc agc aca gcg aag ggg gaa tcc cat acg cac 160
 Glu Val Arg Ile Leu Phe Ser Thr Ala Lys Gly Glu Ser His Thr His
 10 15 20

aag gca ggc ttc aag cag cta ttt cga cga ttg cgt tca act tat cgt 208
 Lys Ala Gly Phe Lys Gln Leu Phe Arg Arg Leu Arg Ser Thr Tyr Arg
 25 30 35

cca gac aaa gta gat aag gat gac ttc acg ctg gac acg ctg cggt tca 256
 Pro Asp Lys Val Asp Lys Asp Asp Phe Thr Leu Asp Thr Leu Arg Ser
 40 45 50 55

gcg cac atc ctt gtg ctc ggt ggc ccg aag gag aag ttc acc gcg cct 304
 Ala His Ile Leu Val Leu Gly Gly Pro Lys Glu Lys Phe Thr Ala Pro
 60 65 70

gag gtg gac atg ctc aaa aag ttc gtg aag aat ggt ggc tcc atc ctc 352
 Glu Val Asp Met Leu Lys Lys Phe Val Lys Asn Gly Gly Ser Ile Leu
 75 80 85

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 Ile Leu Met Ser Glu Gly Glu Glu Lys Ala Gly Thr Asn Ile Asn
 90 95 100

tac ttc ctc gag cag ttt ggc atg tcg gtg aac aac gac gcc gtg gtc 448
 Tyr Phe Leu Glu Gln Phe Gly Met Ser Val Asn Asn Asp Ala Val Val
 105 110 115

cgc acc acg cac tac aag tac ctg cac ccc aag gag gtg ctc atc tcg 496
 Arg Thr Thr His Tyr Lys Tyr Leu His Pro Lys Glu Val Leu Ile Ser
 120 125 130 135

gac ggc atc ctc aac cg ^g gc ^g gt ^g atc ac ^g gg ^c gc ^g gg ^g aag tc ^g ct ^g	544
Asp Gly Ile Leu Asn Arg Ala Val Ile Thr Gly Ala Gly Lys Ser Leu	
140 145 150	
aac agc aac gac gac gag ttc cg ^c gt ^g tc ^g cg ^g gg ^g cc ^g ca ^g gc ^t	592
Asn Ser Asn Asp Asp Asp Glu Phe Arg Val Ser Arg Gly Pro Gln Ala	
155 160 165	
ttt gat ggc ac ^g gg ^c ct ^g gag tac gtc ttc ccc ttc ggt gg ^c ac ^g ct ^c	640
Phe Asp Gly Thr Gly Leu Glu Tyr Val Phe Pro Phe Gly Ala Thr Leu	
170 175 180	
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Ser Val Gln Lys Pro Ala Val Pro Val Leu Ser Ser Gly Lys Ile Ala	
185 190 195	
ta ^c cc ^c at ^g aa ^c cg ^g cc ^a gt ^g gg ^t gc ^g gt ^a tg ^g gg ^c ca ^g cc ^c gg ^c ta ^c	736
Tyr Pro Met Asn Arg Pro Val Gly Ala Val Trp Ala Gln Pro Gly Tyr	
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Gly Arg Ile Ala Val Leu Gly Ser Cys Ala Met Phe Asp Asp Lys Trp	
220 225 230	
ct ^g ga ^c aa ^g ga ^g aa ^c tc ^c aa ^a at ^c at ^g ga ^c tt ^c tt ^c tt ^c aag tt ^c	832
Leu Asp Lys Glu Glu Asn Ser Lys Ile Met Asp Phe Phe Phe Lys Phe	
235 240 245	
ct ^c ga ^g cc ^g ca ^t tc ^c aa ^a at ^c ca ^a gg ^c at ^g ga ^c gg ^g ga ^g	880
Leu Glu Pro His Ser Lys Ile Gln Leu Asn Asp Ile Asp Ala Glu Glu	
250 255 260	
cc ^g ga ^c gt ^g ag ^c ga ^c ct ^g aa ^g ct ^g cc ^c ga ^c aca gg ^c ag ^t ct ^g ga ^c	928
Pro Asp Val Ser Asp Leu Lys Leu Leu Pro Asp Thr Ala Ser Leu Ala	
265 270 275	
ga ^c aa ^g ct ^g aa ^g gg ^c tg ^c ct ^c ca ^g ga ^g at ^c ga ^c gt ^g cc ^g cg ^c ga ^c	976
Asp Lys Leu Lys Gly Cys Leu Gln Glu Ile Asp Asp Val Pro Arg Asp	
280 285 290 295	
tg ^g acc tc ^g ct ^g tt ^c ga ^c tg ^c ct ^g tt ^c aag tt ^c ga ^c ac ^c gg ^c ct ^c	1024
Trp Thr Ser Leu Phe Asp Asp Ser Leu Phe Lys Phe Asp Thr Gly Leu	
300 305 310	
at ^c ct ^t ga ^c gg ^c gt ^g ct ^g ct ^g ta ^c ga ^g ct ^g gg ^c gt ^g aag aag gg ^g	1072
Ile Pro Glu Ala Val Ser Leu Tyr Glu Lys Leu Gly Val Lys Lys Gly	
315 320 325	
ca ^g ct ^g aa ^c ct ^c at ^c cc ^g cc ^c tc ^c ga ^g ac ^g cc ^a ct ^g cc ^g cc ^c ct ^g	1120
Gln Leu Asn Leu Ile Pro Pro Ser Phe Glu Thr Pro Leu Pro Pro Leu	
330 335 340	
ca ^g cc ^c gg ^c gt ^g tt ^c cc ^g cc ^c ac ^c at ^c cg ^t ga ^g cc ^g cc ^c cc ^g gg ^c	1168
Gln Pro Ala Val Phe Pro Pro Thr Ile Arg Glu Pro Pro Pro Pro Ala	
345 350 355	

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 Leu Glu Leu Phe Asp Leu Asp Glu Ser Phe Ala Ser Glu Thr Asn Arg
 360 365 370 375

ctg gcc tcg ctc acc aac aag tgc cac ggc gag gag gac ctg gag tac 1264
 Leu Ala Ser Leu Thr Asn Lys Cys His Gly Glu Glu Asp Leu Glu Tyr
 380 385 390

tac atc atg gag gcg ggc cac atc ctg ggc ctc aag ctg cag gag aac 1312
 Tyr Ile Met Glu Ala Gly His Ile Leu Gly Leu Lys Leu Gln Glu Asn
 395 400 405

gcc aac gcc aag cac gtg tcg gag gtg ttc cgc cgc atc gcg cag 1360
 Ala Asn Ala Lys His Val Leu Ser Glu Val Phe Arg Arg Ile Ala Gln
 410 415 420

tac aag atg ggc agc ctg ggc ctc aag acg ctg gac tcc atg ggc 1408
 Tyr Lys Met Gly Ser Leu Gly Leu Gln Thr Leu Asp Ser Met Gly
 425 430 435

cag acc ctg ccc gcg gcc aac cag ttc ggc gac cag ttc gag ctg 1453
 Gln Thr Leu Pro Ala Ala Asn Gln Phe Gly Asp Gln Phe Glu Leu
 440 445 450

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 35 40 45
 Thr Leu Asp Thr Leu Arg Ser Ala His Ile Leu Val Leu Gly Gly Pro
 50 55 60

Lys Glu Lys Phe Thr Ala Pro Glu Val Asp Met Leu Lys Lys Phe Val
 65 70 75 80
 Lys Asn Gly Gly Ser Ile Leu Ile Leu Met Ser Glu Gly Gly Glu Glu
 85 90 95
 Lys Ala Gly Thr Asn Ile Asn Tyr Phe Leu Glu Gln Phe Gly Met Ser
 100 105 110
 Val Asn Asn Asp Ala Val Val Arg Thr Thr His Tyr Lys Tyr Leu His
 115 120 125
 Pro Lys Glu Val Leu Ile Ser Asp Gly Ile Leu Asn Arg Ala Val Ile
 130 135 140
 Thr Gly Ala Gly Lys Ser Leu Asn Ser Asn Asp Asp Asp Glu Phe Arg
 145 150 155 160
 Val Ser Arg Gly Pro Gln Ala Phe Asp Gly Thr Gly Leu Glu Tyr Val
 165 170 175
 Phe Pro Phe Gly Ala Thr Leu Ser Val Gln Lys Pro Ala Val Pro Val
 180 185 190
 Leu Ser Ser Gly Lys Ile Ala Tyr Pro Met Asn Arg Pro Val Gly Ala
 195 200 205
 Val Trp Ala Gln Pro Gly Tyr Gly Arg Ile Ala Val Leu Gly Ser Cys
 210 215 220
 Ala Met Phe Asp Asp Lys Trp Leu Asp Lys Glu Glu Asn Ser Lys Ile
 225 230 235 240
 Met Asp Phe Phe Lys Phe Leu Glu Pro His Ser Lys Ile Gln Leu
 245 250 255
 Asn Asp Ile Asp Ala Glu Glu Pro Asp Val Ser Asp Leu Lys Leu Leu
 260 265 270
 Pro Asp Thr Ala Ser Leu Ala Asp Lys Leu Lys Gly Cys Leu Gln Glu
 275 280 285
 Ile Asp Asp Val Pro Arg Asp Trp Thr Ser Leu Phe Asp Asp Ser Leu
 290 295 300
 Phe Lys Phe Asp Thr Gly Leu Ile Pro Glu Ala Val Ser Leu Tyr Glu
 305 310 315 320
 Lys Leu Gly Val Lys Lys Gly Gln Leu Asn Leu Ile Pro Pro Ser Phe
 325 330 335
 Glu Thr Pro Leu Pro Pro Leu Gln Pro Ala Val Phe Pro Pro Thr Ile
 340 345 350
 Arg Glu Pro Pro Pro Pro Ala Leu Glu Leu Phe Asp Leu Asp Glu Ser
 355 360 365

a)
 Phe Ala Ser Glu Thr Asn Arg Leu Ala Ser Leu Thr Asn Lys Cys His
 370 375 380
 Gly Glu Glu Asp Leu Glu Tyr Tyr Ile Met Glu Ala Gly His Ile Leu
 385 390 395 400
 Gly Leu Lys Leu Gln Glu Asn Ala Asn Ala Lys His Val Leu Ser Glu
 405 410 415
 Val Phe Arg Arg Ile Ala Gln Tyr Lys Met Gly Ser Leu Gly Leu Gly
 420 425 430
 Gln Thr Leu Asp Ser Met Gly Gln Thr Leu Pro Ala Ala Asn Gln Phe
 435 440 445
 Gly Asp Gln Phe Glu Leu
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<210> 9
 <211> 1902
 <212> DNA
 <213> Chlamydomonas reinhardtii

<220>
<221> CDS
<222> (86) ... (1492)

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ccgttagattc atttaagcga gagac atg agc agc aag cgg ggt ggg cgg tca 112
Met Ser Ser Lys Arg Gly Gly Arg Ser
1 5
tcc tta gca aag gcg ccc gaa gag gcg gta aat ggc gag gca ttt gcg 160
Ser Leu Ala Lys Ala Pro Glu Glu Ala Val Asn Gly Glu Ala Phe Ala
10 15 20 25
cct gag gca tct ccc cct cca ccc ggc gac gat gga gat gct ggt ggg 208
Pro Glu Ala Ser Pro Pro Pro Gly Asp Asp Gly Asp Ala Gly Gly
30 35 40
gag gac ggt ggc gcg cct gcg ccc cct ccg ccc ccg gct aca aag ggc 256
Glu Asp Gly Gly Ala Pro Ala Pro Pro Pro Pro Ala Thr Lys Gly
45 50 55
ggc gat ttc tgc agg aag aag ccc tac cgg aaa ccc ctc tcg cgg 304
Gly Pro Val Ala Val Gly Arg Ser Leu Glu Ile Gln Thr Thr Pro Asp
60 65 70
gtg tgc atg gaa atg ctg gcc gac aag ctg aag ctg cta aac tac gag 352
Val Cys Met Glu Met Leu Ala Asp Lys Leu Lys Leu Leu Asn Tyr Glu
75 80 85
gcg gat ttc tgc agg aag aag ccc tac cgg aaa ccc ctc tcg cgg 400
Ala Asp Phe Cys Arg Lys Lys Pro Tyr Arg Lys Pro Leu Ser Arg
90 95 100 105
ctc tat ttt gcg gtg ccg ctc gca aac tcg agc gag cag ttc ttc tac 448
Leu Tyr Phe Ala Val Pro Leu Ala Asn Ser Ser Glu Gln Phe Phe Tyr
110 115 120
ttt acc agt ctg gcg acc tgg ctg ctg ggc ctg gct ggc gtg gag ctg 496
Phe Thr Ser Leu Ala Thr Trp Leu Leu Gly Leu Ala Gly Val Glu Leu
125 130 135
ccc gct ccc aag gag ttt gat gac ccg aac ttg acg tgc cag aac atc 544
Pro Ala Pro Lys Glu Phe Asp Asp Pro Asn Leu Thr Cys Gln Asn Ile
140 145 150
ctg ggt gcg gtg aag aag ctg ggc ttt gcg ccg ccc agc tac cac cct 592
Leu Gly Ala Val Lys Lys Leu Gly Phe Ala Pro Pro Ser Tyr His Pro
155 160 165
acc aag ctc aca gtg ggc aac ggc aag gag gtg gtg ggt gtg ctg gac 640
Thr Lys Leu Thr Val Gly Asn Gly Lys Glu Val Val Gly Val Leu Asp
170 175 180 185

ggc ctg gtg gac ttc gtg ctg gag cgg cg	cac cac aag tac agc cg	688	
Gly Leu Val Asp Phe Val Leu Glu Arg Arg His His Lys Tyr Ser Arg			
190	195	200	
ccc gcg tac gga aat gat ggg caa ccg gag gag ggc gtg caa ctg gac		736	
Pro Ala Tyr Gly Asn Asp Gly Gln Pro Glu Glu Gly Val Gln Leu Asp			
205	210	215	
gat gag gcg gag gct gcc gcg atg gag ggt gcg gat gag ctg gcg atg		784	
Asp Glu Ala Glu Ala Ala Met Glu Gly Ala Asp Glu Leu Ala Met			
220	225	230	
cca gcc cag aac cag gcg gat gac gat gag gag gag ggc gta tac		832	
Pro Ala Gln Asn Gln Ala Asp Asp Asp Glu Glu Glu Gly Val Tyr			
235	240	245	
gtg gac ccg ggg cgc ggt gac gcc gcg ggc cca ggg aca ggg gca tcc		880	
Val Asp Pro Gly Arg Gly Asp Ala Ala Gly Pro Gly Thr Gly Ala Ser			
250	255	260	265
gcg gcg atg gac gcg gag aag gcg gtg ctt gtg tcc aag gtg gac ccc		928	
Ala Ala Met Asp Ala Glu Lys Ala Val Leu Val Ser Lys Val Asp Pro			
270	275	280	
acg ctc tgg aag atc gag ctg gag cgc gtg gcg ccg aag ctg cgt atc		976	
Thr Leu Trp Lys Ile Glu Leu Glu Arg Val Ala Pro Lys Leu Arg Ile			
285	290	295	
acc atc gcc gcc gac tcg aag gac tgg cgc tca cat ctg gat gag gcg		1024	
Thr Ile Ala Ala Asp Ser Lys Asp Trp Arg Ser His Leu Asp Glu Ala			
300	305	310	
cac cag cac aag gag gtg atc agc aag gcc tgg ccc gac agc aag acg		1072	
His Gln His Lys Glu Val Ile Ser Lys Ala Trp Pro Asp Ser Lys Thr			
315	320	325	
tcg ctg gag cgc ctg cgt gcg gac ctg aac ggc acg ctg gag aag ctg		1120	
Ser Leu Glu Arg Leu Arg Ala Asp Leu Asn Gly Thr Leu Glu Lys Leu			
330	335	340	345
cag acg cgt gag aag ttc ctc aac gag cag ttt gag agc ctc atg cag		1168	
Gln Thr Arg Glu Lys Phe Leu Asn Glu Gln Phe Glu Ser Leu Met Gln			
350	355	360	
cag tac cgc gcc gcc cgc acc acg ttc acg gac gtg cag gag aca tac		1216	
Gln Tyr Arg Ala Ala Arg Thr Thr Phe Thr Asp Val Gln Glu Thr Tyr			
365	370	375	
aac cgc aag acg gag gcg gtg gcg gac cgg aac cag gag atg cac cgc		1264	
Asn Arg Lys Thr Glu Ala Val Ala Asp Arg Asn Gln Glu Met His Arg			
380	385	390	
atc ggc gag acg ctg gag gag gtg aag gcc atg atg gac gag aag ggc		1312	
Ile Gly Glu Thr Leu Glu Glu Val Lys Ala Met Met Asp Glu Lys Gly			
395	400	405	

agc aac atc gcg gac gcc acg cct gtg gct cgc atc aag acc gcc atc Ser Asn Ile Ala Asp Ala Thr Pro Val Ala Arg Ile Lys Thr Ala Ile 410 415 420 425	1360
aag cag ctt aac aag gag ctg cac gac atg gag gtg cgc atc ggc gtg Lys Gln Leu Asn Lys Glu Leu His Asp Met Glu Val Arg Ile Gly Val 430 435 440	1408
gtt agc cac acg ctg ctg cag cta tcg ctg cgc aac aag cga ttg ctg Val Ser His Thr Leu Leu Gln Leu Ser Leu Arg Asn Lys Arg Leu Leu 445 450 455	1456
cag gcg cag gcg gct ctc agt gac gag gag gag gac tagctagatc Gln Ala Gln Ala Ala Leu Ser Asp Glu Glu Glu Asp 460 465	1502
agcgagtgac agagggcatg tgtgcgtacc gtgtgcgcgg gtacagccgt gggatggaag aggtgatgtg gcgggttgcg gacccagcat tcggtagacc agatcactta taggtacaga aagacggcta tattgttggg ggcggcgcac cctggctatg tatataacaag ccgtacgc gagccgctgc aaatgcggtg ctgtgcctgt gctccctgg gtgtgcggcg ttccggtcaa gttcatataa gctgttgtga ctgtgtgaggc aggcatggca tatggacagg gcatccctgc aaggaaagca ggcagcggta tccttgtgg gatgggtcaa gcagtgtatgg aggggcgaag cgagttgcgg gcctgtaaac acagggttgc caaaaaaaaaaaaaaaa 1562 1622 1682 1742 1802 1862 1902	
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<400> 10 Met Ser Ser Lys Arg Gly Gly Arg Ser Ser Leu Ala Lys Ala Pro Glu 1 5 10 15 Glu Ala Val Asn Gly Glu Ala Phe Ala Pro Glu Ala Ser Pro Pro Pro 20 25 30 Pro Gly Asp Asp Gly Asp Ala Gly Gly Glu Asp Gly Gly Ala Pro Ala 35 40 45 Pro Pro Pro Pro Ala Thr Lys Gly Gly Pro Val Ala Val Gly Arg 50 55 60 Ser Leu Glu Ile Gln Thr Thr Pro Asp Val Cys Met Glu Met Leu Ala 65 70 75 80 Asp Lys Leu Lys Leu Leu Asn Tyr Glu Ala Asp Phe Cys Arg Lys Lys 85 90 95 Lys Pro Tyr Arg Lys Pro Leu Ser Arg Leu Tyr Phe Ala Val Pro Leu 100 105 110 Ala Asn Ser Ser Glu Gln Phe Phe Tyr Phe Thr Ser Leu Ala Thr Trp 115 120 125 Leu Leu Gly Leu Ala Gly Val Glu Leu Pro Ala Pro Lys Glu Phe Asp 130 135 140 Asp Pro Asn Leu Thr Cys Gln Asn Ile Leu Gly Ala Val Lys Lys Leu 145 150 155 160 Gly Phe Ala Pro Pro Ser Tyr His Pro Thr Lys Leu Thr Val Gly Asn 165 170 175 Gly Lys Glu Val Val Gly Val Leu Asp Gly Leu Val Asp Phe Val Leu 180 185 190 Glu Arg Arg His His Lys Tyr Ser Arg Pro Ala Tyr Gly Asn Asp Gly 195 200 205	

Gln Pro Glu Glu Gly Val Gln Leu Asp Asp Glu Ala Glu Ala Ala Ala
 210 215 220
 Met Glu Gly Ala Asp Glu Leu Ala Met Pro Ala Gln Asn Gln Ala Asp
 225 230 235 240
 Asp Asp Glu Glu Glu Gly Val Tyr Val Asp Pro Gly Arg Gly Asp
 245 250 255
 Ala Ala Gly Pro Gly Thr Gly Ala Ser Ala Ala Met Asp Ala Glu Lys
 260 265 270
 Ala Val Leu Val Ser Lys Val Asp Pro Thr Leu Trp Lys Ile Glu Leu
 275 280 285
 Glu Arg Val Ala Pro Lys Leu Arg Ile Thr Ile Ala Ala Asp Ser Lys
 290 295 300
 Asp Trp Arg Ser His Leu Asp Glu Ala His Gln His Lys Glu Val Ile
 305 310 315 320
 Ser Lys Ala Trp Pro Asp Ser Lys Thr Ser Leu Glu Arg Leu Arg Ala
 325 330 335
 Asp Leu Asn Gly Thr Leu Glu Lys Leu Gln Thr Arg Glu Lys Phe Leu
 340 345 350
 Asn Glu Gln Phe Glu Ser Leu Met Gln Gln Tyr Arg Ala Ala Arg Thr
 355 360 365
 Thr Phe Thr Asp Val Gln Glu Thr Tyr Asn Arg Lys Thr Glu Ala Val
 370 375 380
 Ala Asp Arg Asn Gln Glu Met His Arg Ile Gly Glu Thr Leu Glu Glu
 385 390 395 400
 Val Lys Ala Met Met Asp Glu Lys Gly Ser Asn Ile Ala Asp Ala Thr
 405 410 415
 Pro Val Ala Arg Ile Lys Thr Ala Ile Lys Gln Leu Asn Lys Glu Leu
 420 425 430
 His Asp Met Glu Val Arg Ile Gly Val Val Ser His Thr Leu Leu Gln
 435 440 445
 Leu Ser Leu Arg Asn Lys Arg Leu Leu Gln Ala Gln Ala Ala Leu Ser
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 Asp Glu Glu Glu Asp
 465

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 <211> 1559
 <212> DNA
 <213> Mus musculus

<220>
 <221> CDS
 <222> (59)...(1345)

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 atg gcc gcc gcg gcc gtc atc ccg ccg tcg ggc ttg gac gat ggg 106
 Met Ala Ala Ala Ala Val Ile Pro Pro Ser Gly Leu Asp Asp Gly
 1 5 10 15
 gtg tct cgg gct cgc ggg gaa ggc gca ggg gag gct gtc gtc gag cgc 154
 Val Ser Arg Ala Arg Gly Glu Gly Ala Gly Glu Ala Val Val Glu Arg
 20 25 30
 ggg cca gga gcg gcc tac cac atg ttc gtc gtc atg gaa gac tta gtc 202
 Gly Pro Gly Ala Ala Tyr His Met Phe Val Val Met Glu Asp Leu Val
 35 40 45

gag aag ctg aag ctg ctc cgc tac gag gag gag cta ctc cga aag agc Glu Lys Leu Lys Leu Leu Arg Tyr Glu Glu Leu Leu Arg Lys Ser	250
50 55 60	
aat ctg aag ccc ccg tcc aga cac tac ttt gct ctg cct acc aac cca Asn Leu Lys Pro Pro Ser Arg His Tyr Phe Ala Leu Pro Thr Asn Pro	298
65 70 75 80	
ggc gag cag ttc tac atg ttt tgc act ctt gct gcg tgg ctg atc aac Gly Glu Gln Phe Tyr Met Phe Cys Thr Leu Ala Ala Trp Leu Ile Asn	346
85 90 95	
aaa act ggc cgt gcc ttt gag cag cct caa gaa tac gac gat ccc aat Lys Thr Gly Arg Ala Phe Glu Gln Pro Gln Glu Tyr Asp Asp Pro Asn	394
100 105 110	
gca act ata tct aat ata ctc tct gag ctt cgc tct ttt ggg aga act Ala Thr Ile Ser Asn Ile Leu Ser Glu Leu Arg Ser Phe Gly Arg Thr	442
115 120 125	
gca gat ttt cct cct tca aaa tta aag tct ggt tac gga gaa caa gtg Ala Asp Phe Pro Pro Ser Lys Leu Lys Ser Gly Tyr Gly Glu Gln Val	490
130 135 140	
<i>A</i> tgc tat gtt ctt gat tgc tta gct gaa gaa gct tta aaa tat att ggt Cys Tyr Val Leu Asp Cys Leu Ala Glu Glu Ala Leu Lys Tyr Ile Gly	538
145 150 155 160	
ttc act tgg aaa agg cca tca tac cca gtg gaa gaa cta gaa gaa Phe Thr Trp Lys Arg Pro Ser Tyr Pro Val Glu Glu Leu Glu Glu Glu	586
165 170 175	
act gtt cca gaa gat gat gcc gag tta aca tta agt aaa gtg gat gaa Thr Val Pro Glu Asp Asp Ala Glu Leu Thr Leu Ser Lys Val Asp Glu	634
180 185 190	
gaa ttt gtg gaa gag gag aca gat aat gaa gaa aac ttt att gat ctc Glu Phe Val Glu Glu Glu Thr Asp Asn Glu Glu Asn Phe Ile Asp Leu	682
195 200 205	
aac gtt tta aag gcc cag acc tat cgc ttg gac aca aac gag tct gcc Asn Val Leu Lys Ala Gln Thr Tyr Arg Leu Asp Thr Asn Glu Ser Ala	730
210 215 220	
aaa caa gaa gat att ttg gaa tct acg aca gat gct gcg gaa tgg agc Lys Gln Glu Asp Ile Leu Glu Ser Thr Thr Asp Ala Ala Glu Trp Ser	778
225 230 235 240	
cta gaa gtt gag cgt gta cta ccg cag ctg aaa gtc acg att agg act Leu Glu Val Glu Arg Val Leu Pro Gln Leu Lys Val Thr Ile Arg Thr	826
245 250 255	
gac aat aag gat tgg agg atc cat gtt gac caa atg cac cag cac aaa Asp Asn Lys Asp Trp Arg Ile His Val Asp Gln Met His Gln His Lys	874
260 265 270	

agt ggg att gaa tct gct ctg aag gag acc aag ggg ttt ttg gac aag 922
 Ser Gly Ile Glu Ser Ala Leu Lys Glu Thr Lys Gly Phe Leu Asp Lys
 275 280 285

ctc cat aat gaa att agc agg act ctg gaa aag att ggc agc cga gaa 970
 Leu His Asn Glu Ile Ser Arg Thr Leu Glu Lys Ile Gly Ser Arg Glu
 290 295 300

aag tac att aac aat caa ctt gag cac ttg gtt caa gaa tat cgt ggg 1018
 Lys Tyr Ile Asn Asn Gln Leu Glu His Leu Val Gln Glu Tyr Arg Gly
 305 310 315 320

gcc caa gcc cag cta agt gag gca agg gag cgc tac cag cag ggc aat 1066
 Ala Gln Ala Gln Leu Ser Glu Ala Arg Glu Arg Tyr Gln Gln Gly Asn
 325 330 335

ggc gga gta act gaa cg^g acc aga ctc ctc tct gag gtt aca gaa gaa 1114
 Gly Gly Val Thr Glu Arg Thr Arg Leu Leu Ser Glu Val Thr Glu Glu
 340 345 350

tta gaa aag gta aag caa gaa atg gaa gag aag ggc agc agc atg acg 1162
 Leu Glu Lys Val Lys Gln Glu Met Glu Glu Lys Gly Ser Ser Met Thr
 355 360 365

gac ggc act cct ttg gtg aag att aag cag agc tta acc aag ctg aag 1210
 Asp Gly Thr Pro Leu Val Lys Ile Lys Gln Ser Leu Thr Lys Leu Lys
 370 375 380

Ak
 caa gaa act gtt cag atg gac att aga atc ggt gtg gtg gag cac acg 1258
 Gln Glu Thr Val Gln Met Asp Ile Arg Ile Gly Val Val Glu His Thr
 385 390 395 400

cta ctt cag tca aaa ctc aag gag aag tgc aac atg acc agg gac atg 1306
 Leu Leu Gln Ser Lys Leu Lys Glu Lys Cys Asn Met Thr Arg Asp Met
 405 410 415

cat gca gct gtc acc cca gag tca gca att ggc ttc tat taaacacgtg 1355
 His Ala Ala Val Thr Pro Glu Ser Ala Ile Gly Phe Tyr
 420 425

ggcttccatg cttctgatta tttcgaaaaatg attttttaat gttgcattga 1415
 tttccaaaca caatttatac ttcttcaagc atattcagtg ggtatTTTg cacatgtgtt
 aatatcatgg tgattatgat ggc^{aa}agcc tgtacaatga atatagtatt taataaaagta 1475
 cttaaaaatta aaaaaaaaaaaa aaaa 1535
 1559

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 <211> 429
 <212> PRT
 <213> Mus musculus

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 20 25 30
 Gly Pro Gly Ala Ala Tyr His Met Phe Val Val Met Glu Asp Leu Val
 35 40 45

Glu Lys Leu Lys Leu Leu Arg Tyr Glu Glu Glu Leu Leu Arg Lys Ser
 50 55 60
 Asn Leu Lys Pro Pro Ser Arg His Tyr Phe Ala Leu Pro Thr Asn Pro
 65 70 75 80
 Gly Glu Gln Phe Tyr Met Phe Cys Thr Leu Ala Ala Trp Leu Ile Asn
 85 90 95
 Lys Thr Gly Arg Ala Phe Glu Gln Pro Gln Glu Tyr Asp Asp Pro Asn
 100 105 110
 Ala Thr Ile Ser Asn Ile Leu Ser Glu Leu Arg Ser Phe Gly Arg Thr
 115 120 125
 Ala Asp Phe Pro Pro Ser Lys Leu Lys Ser Gly Tyr Gly Glu Gln Val
 130 135 140
 Cys Tyr Val Leu Asp Cys Leu Ala Glu Glu Ala Leu Lys Tyr Ile Gly
 145 150 155 160
 Phe Thr Trp Lys Arg Pro Ser Tyr Pro Val Glu Glu Leu Glu Glu Glu
 165 170 175
 Thr Val Pro Glu Asp Asp Ala Glu Leu Thr Leu Ser Lys Val Asp Glu
 180 185 190
 Glu Phe Val Glu Glu Glu Thr Asp Asn Glu Glu Asn Phe Ile Asp Leu
 195 200 205
 Asn Val Leu Lys Ala Gln Thr Tyr Arg Leu Asp Thr Asn Glu Ser Ala
 210 215 220
 Lys Gln Glu Asp Ile Leu Glu Ser Thr Thr Asp Ala Ala Glu Trp Ser
 225 230 235 240
 Leu Glu Val Glu Arg Val Leu Pro Gln Leu Lys Val Thr Ile Arg Thr
 245 250 255
 Asp Asn Lys Asp Trp Arg Ile His Val Asp Gln Met His Gln His Lys
 260 265 270
 Ser Gly Ile Glu Ser Ala Leu Lys Glu Thr Lys Gly Phe Leu Asp Lys
 275 280 285
 Leu His Asn Glu Ile Ser Arg Thr Leu Glu Lys Ile Gly Ser Arg Glu
 290 295 300
 Lys Tyr Ile Asn Asn Gln Leu Glu His Leu Val Gln Glu Tyr Arg Gly
 305 310 315 320
 Ala Gln Ala Gln Leu Ser Glu Ala Arg Glu Arg Tyr Gln Gln Gly Asn
 325 330 335
 Gly Gly Val Thr Glu Arg Thr Arg Leu Leu Ser Glu Val Thr Glu Glu
 340 345 350
 Leu Glu Lys Val Lys Gln Glu Met Glu Glu Lys Gly Ser Ser Met Thr
 355 360 365
 Asp Gly Thr Pro Leu Val Lys Ile Lys Gln Ser Leu Thr Lys Leu Lys
 370 375 380
 Gln Glu Thr Val Gln Met Asp Ile Arg Ile Gly Val Val Glu His Thr
 385 390 395 400
 Leu Leu Gln Ser Lys Leu Lys Glu Lys Cys Asn Met Thr Arg Asp Met
 405 410 415
 His Ala Ala Val Thr Pro Glu Ser Ala Ile Gly Phe Tyr
 420 425

<210> 13

<211> 1954

<212> DNA

<213> Chlamydomonas reinhardtii

<220>

<221> CDS

<222> (1) ... (1302)

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cag cag cgc aag cgc gtg gac gag gtg ctc acg gag cgc ctc aac ctc 96
 Gln Gln Arg Lys Arg Val Asp Glu Val Leu Thr Glu Arg Leu Asn Leu
 20 25 30

gag tcc aag gcc aag cag gcc gag tcc aag atg tct gag atc cag gcg 144
 Glu Ser Lys Ala Lys Gln Ala Glu Ser Lys Met Ser Glu Ile Gln Ala
 35 40 45

tcc atg gac cag cgc ctc aac tct atg ccg ccc agc cag cgc aac gaa 192
 Ser Met Asp Gln Arg Leu Asn Ser Met Pro Pro Ser Gln Arg Asn Glu
 50 55 60

tac acc acg ctc gtg gcc gag cag cag ctg cag gcc gac agc aag 240
 Tyr Thr Thr Leu Val Ala Glu Gln Gln Leu Gln Ala Asp Ser Lys
 65 70 75 80

cgcc ttg gag gag gtg ctg gac gag ctg gac aag gcg ctg cag gcc agc 288
 Arg Phe Glu Glu Val Leu Asp Glu Leu Asp Lys Ala Leu Gln Ala Ser
 85 90 95

a
 gag ggc gag ctg gcg cgc aac ccc ttc aag cag cgc agc ctg cag ctg 336
 Glu Gly Glu Leu Ala Arg Asn Pro Phe Lys Gln Arg Ser Leu Gln Leu
 100 105 110

cag gag cag atc cgc gcg ctc acg ggg aag aag tac gag ctg acg gag 384
 Gln Glu Gln Ile Arg Ala Leu Thr Gly Lys Lys Tyr Glu Leu Thr Glu
 115 120 125

gag gag cgg cag agc aag cgc tcg ccc gag gag ctg cgc gcc gac ctc 432
 Glu Glu Arg Gln Ser Lys Arg Ser Pro Glu Glu Leu Arg Ala Asp Leu
 130 135 140

atg gcc aag atc aag cga gac aac acc gag gtg gag cag atg acg cag 480
 Met Ala Lys Ile Lys Arg Asp Asn Thr Glu Val Glu Gln Met Thr Gln
 145 150 155 160

cag atc cgc gag ctt cag gac cag atc aag aag atg gag gag cgc gtc 528
 Gln Ile Arg Glu Leu Gln Asp Gln Ile Lys Lys Met Glu Glu Arg Val
 165 170 175

aag agc ctg ggc ggc gcc acc agc ggc gcg gtg gcg gcg gag gaa aag 576
 Lys Ser Leu Gly Gly Ala Thr Ser Gly Ala Val Ala Ala Glu Glu Lys
 180 185 190

gcc aac cgc gag aag ttt gag gag ctg ttg gcc aag gag cgc cac cta 624
 Ala Asn Arg Glu Lys Phe Glu Glu Leu Leu Ala Lys Glu Arg His Leu
 195 200 205

aac aac ttt atg gac ggc ttc ccc agc cgc aag gcc gac aag atg cag 672
 Asn Asn Phe Met Asp Gly Phe Pro Ser Arg Lys Ala Ala Lys Met Gln
 210 215 220

gag aag cag cag aag gag gac ggc atc gtg ggc gtg ctg gag aag atg Glu Lys Gln Gln Lys Glu Asp Gly Ile Val Gly Val Leu Glu Lys Met 225 230 235 240	720
gtg aag atg cag ggc atc att ggc tcc aac ctg ccc agc cag aag aag Val Lys Met Gln Gly Ile Ile Gly Ser Asn Leu Pro Ser Gln Lys Lys 245 250 255	768
tac aag gaa atg cag gac gag ctc gag tac aag aag atg cag ctg gag Tyr Lys Glu Met Gln Asp Glu Leu Glu Tyr Lys Lys Met Gln Leu Glu 260 265 270	816
aac acg cag acc acg cag gag cg ^g ctc aag gag gag ctg acc atg cg ^g Asn Thr Gln Thr Gln Glu Arg Leu Lys Glu Glu Leu Thr Met Arg 275 280 285	864
cgc aca gag ctg gag aag atc gat acg ctg gag gac aag atc aag ctg Arg Thr Glu Leu Glu Lys Ile Asp Thr Leu Glu Asp Lys Ile Lys Leu 290 295 300	912
gag ctg acg cag ctg gc ^g gag cg ^g cag gag gcc atg gag aag gag atg Glu Leu Thr Gln Leu Ala Glu Arg Gln Glu Ala Met Glu Lys Glu Met 305 310 315 320	960
ggc gag ttc ggc agc gtc gag gac atc cag cg ^c aag gcc aac gcc gca Gly Glu Phe Gly Ser Val Glu Asp Ile Gln Arg Lys Ala Asn Ala Ala 325 330 335	1008
cgc gag cgc atg ggg gcc tgc gca gtg tgc tgt ttg aag cgc aag gac Arg Glu Arg Met Gly Ala Cys Ala Val Cys Cys Leu Lys Arg Lys Asp 340 345 350	1056
ctg ctg cgc tcc atc gtg gc ^g gag cg ^c ggc ctc aag ttc cag gcc aag Leu Leu Arg Ser Ile Val Ala Glu Arg Gly Leu Lys Phe Gln Ala Lys 355 360 365	1104
cgc gc ^g cag ctg cag gac cac aac ctc cag gtg cag ctg gag aag atg Arg Ala Gln Leu Gln Asp His Asn Leu Gln Val Gln Leu Glu Lys Met 370 375 380	1152
gag gcc aag ctg aag aat ctg agc gc ^g ggc gta ttc gag atg gac gag Glu Ala Lys Leu Lys Asn Leu Ser Ala Gly Val Phe Glu Met Asp Glu 385 390 395 400	1200
ttc atc aag gcc aag gag agc gag acc aac tac cgc cag ctg gcc tcc Phe Ile Lys Ala Lys Glu Ser Glu Thr Asn Tyr Arg Gln Leu Ala Ser 405 410 415	1248
aac ata gc ^g gc ^g ctg gta gac gac ctc aac gtg cat gtc aag aag gcc Asn Ile Ala Ala Leu Val Asp Asp Leu Asn Val His Val Lys Lys Ala 420 425 430	1296

gtg gtg taagaaggag gcagtggtgt aaggggtctc cggaggaggg cgcgtgccgt 1352
 Val Val

tgtggggtg ttggggcgc ggcgcgagaa gtacgtgcgt gtggcggtgt gccttcagc	1412
aggctgcacg ttagtacgg tagtcaaggt gaaggccggc ctgggcacag gaggatgctg	1472
acgcgcgtgac gggtgacgt gacaggccat cgcgagttt atctctgctg tcgagtcatt	1532
gacttgggtt cctagacagg tcgggctaca agcccgagg ttgatggctc acctcgcagt	1592
gcgcggacag caggtgtggc gcatgcgcgt gtgcctcagg agcgcgggtgc ggaccaggga	1652
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ccatggcctg gcccgaaggc agcgctcgta gttggatact gaccagcggc gtcaagcggc	1772
gtacgatgtc agaagtggag ctaccgcccc tgacacaagggt gtgatgtaca tactgttatt	1832
taggagtccg ctgcttatag ctactggact gcagaagaag gaggctgcaa ggatctgatg	1892
gaggcgtgg tgtgtatgga tgacgctgta agagatgcac aagagaaaaaaa aaaaaaaaaaa	1952
aa	1954

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 <212> PRT
 <213> Chlamydomonas reinhardtii

A4

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Glu Ser Lys Ala Lys Gln Ala Glu Ser Lys Met Ser Glu Ile Gln Ala		
35 40 45		
Ser Met Asp Gln Arg Leu Asn Ser Met Pro Pro Ser Gln Arg Asn Glu		
50 55 60		
Tyr Thr Thr Leu Val Ala Glu Gln Gln Leu Gln Ala Asp Ser Lys		
65 70 75 80		
Arg Phe Glu Glu Val Leu Asp Glu Leu Asp Lys Ala Leu Gln Ala Ser		
85 90 95		
Glu Gly Glu Leu Ala Arg Asn Pro Phe Lys Gln Arg Ser Leu Gln Leu		
100 105 110		
Gln Glu Gln Ile Arg Ala Leu Thr Gly Lys Lys Tyr Glu Leu Thr Glu		
115 120 125		
Glu Glu Arg Gln Ser Lys Arg Ser Pro Glu Glu Leu Arg Ala Asp Leu		
130 135 140		
Met Ala Lys Ile Lys Arg Asp Asn Thr Glu Val Glu Gln Met Thr Gln		
145 150 155 160		
Gln Ile Arg Glu Leu Gln Asp Gln Ile Lys Lys Met Glu Glu Arg Val		
165 170 175		
Lys Ser Leu Gly Gly Ala Thr Ser Gly Ala Val Ala Ala Glu Glu Lys		
180 185 190		
Ala Asn Arg Glu Lys Phe Glu Glu Leu Leu Ala Lys Glu Arg His Leu		
195 200 205		
Asn Asn Phe Met Asp Gly Phe Pro Ser Arg Lys Ala Ala Lys Met Gln		
210 215 220		
Glu Lys Gln Gln Lys Glu Asp Gly Ile Val Gly Val Leu Glu Lys Met		
225 230 235 240		
Val Lys Met Gln Gly Ile Ile Gly Ser Asn Leu Pro Ser Gln Lys Lys		
245 250 255		
Tyr Lys Glu Met Gln Asp Glu Leu Glu Tyr Lys Lys Met Gln Leu Glu		
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<222> (108) . . . (2453)

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                                         Met Ser Tyr
                                         1

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ggg ggc acg gag gag gat gac ctt tat gga gga tat gat gag caa tcg      164
Gly Gly Thr Glu Glu Asp Asp Leu Tyr Gly Gly Tyr Asp Glu Gln Ser
      5           10          15

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aac ccg ctt gcg ggc tcg ggt ggt gcc gca ttt aag gca ctt ggg gcc      212
Asn Pro Leu Ala Gly Ser Gly Gly Ala Ala Phe Lys Ala Leu Gly Ala
   20          25          30          35

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gat gga gct cct cca ggc acc gcc atg atg ggg ccg cct ggc acg gcc 260
 Asp Gly Ala Pro Pro Gly Thr Ala Met Met Gly Pro Pro Gly Thr Ala
 40 45 50

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atg aag agc ttc gtg cca ggc acg gct atg cgg ggc ggc acg gcg atg      308
Met Lys Ser Phe Val Pro Gly Thr Ala Met Arg Gly Gly Thr Ala Met
          55           60           65

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cag cag gac ccc agc ctg gcg cg⁷⁰ cct atg acc tcg aac cg⁷⁵ ggt gct
 Gln Gln Asp Pro Ser Leu Ala Arg Pro Met Thr Ser Asn Arg Gly Ala
⁷⁰ ⁷⁵ ⁸⁰

ggc ttc acg tcg gcg cct aac aag aag ttt gac ccc ctc aat cgc tca			404
Gly Phe Thr Ser Ala Pro Asn Lys Lys Phe Asp Pro Leu Asn Arg Ser			
85	90	95	
atg ggg tcg aca ctg ggc tcg tcg ggg ggt ggc gca atg ctg gtg gct			452
Met Gly Ser Thr Leu Gly Ser Ser Gly Gly Ala Met Leu Val Ala			
100	105	110	115
cgc aag ggt gac acc agc ccg gag gag cag gcg cgc ggg atg gag aag			500
Arg Lys Gly Asp Thr Ser Pro Glu Glu Gln Ala Arg Gly Met Glu Lys			
120	125	130	
acg gtg cat gag ctg ctt gag aag agc gcg gac gcg gct aag aat			548
Thr Val His Glu Leu Leu Glu Lys Ser Ala Ala Asp Ala Ala Lys Asn			
135	140	145	
gac atc aac tcg gcc ctg gag aac gcc atg gag gcg aag aag aat gag			596
Asp Ile Asn Ser Ala Leu Glu Asn Ala Met Glu Ala Lys Lys Asn Glu			
150	155	160	
cga aag ctg tgc cgc ttc cgg gaa cag aac aac atg gcg gac cag atc			644
Arg Lys Leu Cys Arg Phe Arg Glu Gln Asn Asn Met Ala Asp Gln Ile			
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aac ctg gag ctg atg tac gcc gtg gac ttc aac ctg gca cac atg tac			692
Asn Leu Glu Leu Met Tyr Ala Val Asp Phe Asn Leu Ala His Met Tyr			
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cac atg aac aag aac tac agc gag gcg ctg aac ctg tac aca gca atc			740
His Met Asn Lys Asn Tyr Ser Glu Ala Leu Asn Leu Tyr Thr Ala Ile			
200	205	210	
gtg cgc aac aag aac ttc ccg cag tcg ggt tgg ctg cgc gtc aac atg			788
Val Arg Asn Lys Asn Phe Pro Gln Ser Gly Trp Leu Arg Val Asn Met			
215	220	225	
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Gly Asn Ile His Phe Glu Gln Lys Lys Tyr Pro Ser Ala Ile Lys Met			
230	235	240	
tac cgc atg gcg ttg gac cag atc agc gcc acc gcc aag gag gtc cgc			884
Tyr Arg Met Ala Leu Asp Gln Ile Ser Ala Thr Ala Lys Glu Val Arg			
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ttc aag atc atg cgc aac atc ggg ctg tcg ttc gtg cgc atg ggc cag			932
Phe Lys Ile Met Arg Asn Ile Gly Leu Ser Phe Val Arg Met Gly Gln			
260	265	270	275
tac ccc gac gcg ctg cag tcc ttc gcc acg gtc atg gac aac gtg ccc			980
Tyr Pro Asp Ala Leu Gln Ser Phe Ala Thr Val Met Asp Asn Val Pro			
280	285	290	
gac cac cag acc ggc tac aac ctg gtc atg tgc aac tac gcg ctg agc			1028
Asp His Gln Thr Gly Tyr Asn Leu Val Met Cys Asn Tyr Ala Leu Ser			
295	300	305	

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cgc aag cgc aac acc atc atc acg cgc ctc att gtc aag gcc gcg cag Arg Lys Arg Asn Thr Ile Ile Thr Arg Leu Ile Val Lys Ala Ala Gln 360 365 370	1220
ctc atc tcc gag aag gtg gat cgc gcc aac ggc ttt gag ggc ggc ttc Leu Ile Ser Glu Lys Val Asp Arg Ala Asn Gly Phe Glu Gly Gly Phe 375 380 385	1268
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gcc ggc atc gac ccc tac tgc gtg gag gcc atc tac aac ctg ggc ctg Ala Gly Ile Asp Pro Tyr Cys Val Glu Ala Ile Tyr Asn Leu Gly Leu 500 505 510 515	1652
gtg agc cag cgc ctg aac gag ctg ccg tac gcg ctg gcg gct aag Val Ser Gln Arg Leu Asn Glu Leu Pro Tyr Ala Leu Ala Phe Lys 520 525 530	1700

aag ctg cac aac atg gtg ccc gac aac gtg gag gtc atc cac cag atc Lys Leu His Asn Met Val Pro Asp Asn Val Glu Val Ile His Gln Ile 535 540 545	1748
gcc acc acg tac gac atg atg ggc gac ttc aag aac gcg gtc aag tgg Ala Thr Thr Tyr Asp Met Met Gly Asp Phe Lys Asn Ala Val Lys Trp 550 555 560	1796
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cga ctg gga gcc atc cac gcc agg ttc gac gac gag gcc aag gcg ctg Arg Leu Gly Ala Ile His Ala Arg Phe Asp Asp Glu Ala Lys Ala Leu 580 585 590 595	1892
cac tac tac cag gag tcg cac cgc gtg tac ccg gtg aac atg gac gtc His Tyr Tyr Gln Glu Ser His Arg Val Tyr Pro Val Asn Met Asp Val 600 605 610	1940
atc tcc tgg ctg ggc gcc tac cat gtc aaa tcg gag gtg tac gag aag Ile Ser Trp Leu Gly Ala Tyr His Val Lys Ser Glu Val Tyr Glu Lys 615 620 625	1988
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Lys Glu His Met Gly Gly Gly Gly Lys Asp Asn Asp Asp Trp Gly	
760 765 770	
 aac gag cag ctt ggg gac gac ctg ctg ccc atg taaaccgcag tgctgccaca	2473
Asn Glu Gln Leu Gly Asp Asp Leu Leu Pro Met	
775 780	
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gatggcgagg gcgaggacga cgaccaccta aaagcgctgg ggctgggggt ggggttggtg	2653
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<213> Chlamydomonas reinhardtii

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Gly Thr Ala Met Lys Ser Phe Val Pro Gly Thr Ala Met Arg Gly Gly	
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Thr Ala Met Gln Gln Asp Pro Ser Leu Ala Arg Pro Met Thr Ser Asn	
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85 90 95	
Asn Arg Ser Met Gly Ser Thr Leu Gly Ser Ser Gly Gly Ala Met	
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115 120 125	
Met Glu Lys Thr Val His Glu Leu Leu Glu Lys Ser Ala Ala Asp Ala	
130 135 140	
Ala Lys Asn Asp Ile Asn Ser Ala Leu Glu Asn Ala Met Glu Ala Lys	
145 150 155 160	
Lys Asn Glu Arg Lys Leu Cys Arg Phe Arg Glu Gln Asn Asn Met Ala	
165 170 175	
Asp Gln Ile Asn Leu Glu Leu Met Tyr Ala Val Asp Phe Asn Leu Ala	
180 185 190	
His Met Tyr His Met Asn Lys Asn Tyr Ser Glu Ala Leu Asn Leu Tyr	
195 200 205	

Thr Ala Ile Val Arg Asn Lys Asn Phe Pro Gln Ser Gly Trp Leu Arg
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 Val Asn Met Gly Asn Ile His Phe Glu Gln Lys Lys Tyr Pro Ser Ala
 225 230 235 240
 Ile Lys Met Tyr Arg Met Ala Leu Asp Gln Ile Ser Ala Thr Ala Lys
 245 250 255
 Glu Val Arg Phe Lys Ile Met Arg Asn Ile Gly Leu Ser Phe Val Arg
 260 265 270
 Met Gly Gln Tyr Pro Asp Ala Leu Gln Ser Phe Ala Thr Val Met Asp
 275 280 285
 Asn Val Pro Asp His Gln Thr Gly Tyr Asn Leu Val Met Cys Asn Tyr
 290 295 300
 Ala Leu Ser Asp Arg Glu Gly Met Lys Asn Ala Phe Ile Lys Leu Leu
 305 310 315 320
 Lys Val Ser Pro Ser Ser Glu Met Asp Asp Asp Asp Asp Asp Asp Pro
 325 330 335
 Met Gly Asp Asp Asp Met Gln Val Met Thr Met Asp Asp Gly Leu Lys
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 Asp Glu Met Arg Lys Arg Asn Thr Ile Ile Thr Arg Leu Ile Val Lys
 355 360 365
 Ala Ala Gln Leu Ile Ser Glu Lys Val Asp Arg Ala Asn Gly Phe Glu
 370 375 380
 Gly Gly Phe Met Trp Cys Cys Glu Gln Leu Arg Asp Ala Gly Tyr Thr
 385 390 395 400
 Lys Leu Ala Asn Glu Val Glu Leu Ala Lys Ala Thr Arg Phe Met Gly
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 Gln Lys Gln Phe Asp Lys Ala Val Gly Val Phe Lys Asp Phe Glu Lys
 420 425 430
 Lys Glu Pro Arg Val Lys Ala Arg Ala Ala Thr Asn Leu Ala Phe Leu
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 Tyr Phe Leu Glu Gly Glu Thr Asp Gln Ala Asp Lys Tyr Ser Glu Met
 450 455 460
 Ala Leu Lys Ser Asp Arg Tyr Asn Ala Arg Ala Tyr Val Asn Lys Gly
 465 470 475 480
 Cys Val Leu Val Glu Arg Gly Asp Leu Glu Gly Ala Arg Ser Leu Phe
 485 490 495
 Asn Glu Ala Ala Gly Ile Asp Pro Tyr Cys Val Glu Ala Ile Tyr Asn
 500 505 510
 Leu Gly Leu Val Ser Gln Arg Leu Asn Glu Leu Pro Tyr Ala Leu Ala
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 Ala Phe Lys Lys Leu His Asn Met Val Pro Asp Asn Val Glu Val Ile
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 His Gln Ile Ala Thr Thr Tyr Asp Met Met Gly Asp Phe Lys Asn Ala
 545 550 555 560
 Val Lys Trp Phe Glu Leu Leu Thr Ser Leu Val Ser Asn Asp Pro Gly
 565 570 575
 Val Leu Ala Arg Leu Gly Ala Ile His Ala Arg Phe Asp Asp Glu Ala
 580 585 590
 Lys Ala Leu His Tyr Tyr Gln Glu Ser His Arg Val Tyr Pro Val Asn
 595 600 605
 Met Asp Val Ile Ser Trp Leu Gly Ala Tyr His Val Lys Ser Glu Val
 610 615 620
 Tyr Glu Lys Ala Met Pro Phe Phe Asp Leu Ala Ser Lys Ile Gln Pro
 625 630 635 640
 Gln Glu Val Lys Trp Ala Leu Met Val Ala Ser Cys Tyr Arg Arg Thr
 645 650 655

Asn Asn Leu Pro Ala Ala Leu Gly Lys Tyr Lys Gln Ile His Thr Gln
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 His Pro Asp Asn Val Glu Cys Leu Arg Tyr Leu Val His Leu Cys Ser
 675 680 685
 Glu Leu Gly Arg Arg Ala Glu Ala Ala Glu Tyr Met Thr Lys Leu Lys
 690 695 700
 Lys Ala Glu Lys Ala Ala Val Pro Glu Ala Thr Thr Ala Ala Ala Pro
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 Ala Ala Ala Ala Gly Ser Gly Met Gly Met Gly Gly Leu Asp
 725 730 735
 Asp Asp Ile Gly Ser Ser Ala Val Ser Ala Gln Asn Arg Gly Lys Lys
 740 745 750
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<212> DNA

<213> Chlamydomonas reinhardtii

<220>

<221> CDS

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<400> 17


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 Glu Thr Leu Leu Lys Met Asp Asp Thr Lys Gly Leu Ile Thr Leu Tyr
 20 25 30

gtg gag gct gag aag tgg gat gac gcc ttc ctg ctg cac gcg cac 143
 Val Glu Ala Glu Lys Trp Asp Asp Ala Phe Leu Leu His Ala His
 35 40 45

ccc gag tgc cgg cag gac gtg tac ctg ccc tac gcc aag tgg ctc agc 191
 Pro Glu Cys Arg Gln Asp Val Tyr Leu Pro Tyr Ala Lys Trp Leu Ser
 50 55 60

aac cag gac cgc ttc gat gag gcg cgg ctg gcg tac cag gag ggc ggc 239
 Asn Gln Asp Arg Phe Asp Glu Ala Arg Leu Ala Tyr Gln Glu Gly Gly
 65 70 75

ttt ccc agc ctg gcc acc cgc atc ctg gag cag ttg tgc gcc aac gcg 287
 Phe Pro Ser Leu Ala Thr Arg Ile Leu Glu Gln Leu Cys Ala Asn Ala
 80 85 90 95

gtg gta gag acg cgg tac gac gcc gcc ttc tac tac tat cag ctg 335
 Val Val Glu Thr Arg Tyr Ala Asp Ala Ala Phe Tyr Tyr Tyr Gln Leu
 100 105 110

gcc atg gag gcg ctc aag agc atc aag aac ccg ccc tcc aac atg gcg Ala Met Glu Ala Leu Lys Ser Ile Lys Asn Pro Pro Ser Asn Met Ala 115 120 125	383
ccc tcg gac cgc tcc gcg ctg gag cgc ttc acg gag ctg tac gac cgc Pro Ser Asp Arg Ser Ala Leu Glu Arg Phe Thr Glu Leu Tyr Asp Arg 130 135 140	431
gcc gag gtg tac tac gcc tac gaa gtg gtg cac aag tcc gtg cac tcg Ala Glu Val Tyr Tyr Ala Tyr Glu Val Val His Lys Ser Val His Ser 145 150 155	479
ccc ttc cgc acc acg cac ccc gac acg ctc ttc aac gcc tcg cgc ttc Pro Phe Arg Thr Thr His Pro Asp Thr Leu Phe Asn Ala Ser Arg Phe 160 165 170 175	527
ctg ctc atg cgc ctg ctg ccg ccg cgc gag gtg ccg ctg ggc gtc agc Leu Leu Met Arg Leu Leu Pro Pro Arg Glu Val Pro Leu Gly Val Ser 180 185 190	575
gtg gtc aac gtg gtg tac gtg ctg gcc aag cag gct gtc gag gcg ggc Val Val Asn Val Val Tyr Val Leu Ala Lys Gln Ala Val Glu Ala Gly 195 200 205	623
gcc ttc aag ctg gcg cgc ttc gcg tac aac aag ctg cag acg ctg gtg Ala Phe Lys Leu Ala Arg Phe Ala Tyr Asn Lys Leu Gln Thr Leu Val 210 215 220	671
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ctg ccc gtg gtg gag ttt gag ctg gag ccg ggc gtg gac gac gag gag Leu Pro Val Val Glu Phe Glu Leu Glu Pro Gly Val Asp Asp Glu Glu 290 295 300	911
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gag cgc aag gcg gag cgg cag gcc aag gcg gcg gag gtg ggc ggc aac Glu Arg Lys Ala Glu Arg Gln Ala Lys Ala Ala Glu Val Gly Gly Asn 320 325 330 335	1007

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gcg gcc cag atg gtg ccc aac acc acc atc cgc gtg gac cgg gcc Ala Ala Gln Met Met Val Pro Asn Thr Thr Ile Arg Val Asp Arg Ala 355 360 365	1103
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cgt ggg tgg att ccg gat gta ggc ggg gaa taggagctgc cggttagtggc Arg Gly Trp Ile Pro Asp Val Gly Gly Glu 500 505	1537
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<213> Chlamydomonas reinhardtii

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 Glu Ala Glu Lys Trp Asp Asp Ala Phe Leu Leu Leu His Ala His Pro
 35 40 45
 Glu Cys Arg Gln Asp Val Tyr Leu Pro Tyr Ala Lys Trp Leu Ser Asn
 50 55 60
 Gln Asp Arg Phe Asp Glu Ala Arg Leu Ala Tyr Gln Glu Gly Gly Phe
 65 70 75 80
 Pro Ser Leu Ala Thr Arg Ile Leu Glu Gln Leu Cys Ala Asn Ala Val
 85 90 95
 Val Glu Thr Arg Tyr Ala Asp Ala Ala Phe Tyr Tyr Tyr Gln Leu Ala
 100 105 110
 Met Glu Ala Leu Lys Ser Ile Lys Asn Pro Pro Ser Asn Met Ala Pro
 115 120 125
 Ser Asp Arg Ser Ala Leu Glu Arg Phe Thr Glu Leu Tyr Asp Arg Ala
 130 135 140
 Glu Val Tyr Tyr Ala Tyr Glu Val Val His Lys Ser Val His Ser Pro
 145 150 155 160
 Phe Arg Thr Thr His Pro Asp Thr Leu Phe Asn Ala Ser Arg Phe Leu
 165 170 175
 Leu Met Arg Leu Leu Pro Pro Arg Glu Val Pro Leu Gly Val Ser Val
 180 185 190
 Val Asn Val Val Tyr Val Leu Ala Lys Gln Ala Val Glu Ala Gly Ala
 195 200 205
 Phe Lys Leu Ala Arg Phe Ala Tyr Asn Lys Leu Gln Thr Leu Val Leu
 210 215 220
 Pro Ala Ala Trp Gln Ala Glu Val Asp Leu Ala Ser Val Val Ile Arg
 225 230 235 240
 Ser Lys Pro Phe Ser Asp Lys Glu Asp Leu Leu Pro Val Cys Trp Arg
 245 250 255
 Cys Ser Thr Thr Asn Pro Leu Leu Asn Thr Gln Gly Asp Tyr Cys Ile
 260 265 270
 Asn Cys Gly Ala Pro Phe Ile Arg Ser Phe Val Thr Phe Glu His Leu
 275 280 285
 Pro Val Val Glu Phe Glu Leu Glu Pro Gly Val Asp Asp Glu Glu Ala
 290 295 300
 Gly Arg Leu Leu Gly Glu Asp Ala Gly Met Glu Ala Ala Arg Arg Glu
 305 310 315 320
 Arg Lys Ala Glu Arg Gln Ala Lys Ala Ala Glu Val Gly Gly Asn Met
 325 330 335
 Leu Arg Leu Asp Gln Asn Glu Ile Asp Arg Met Asp Asp Ala Phe Ala
 340 345 350
 Ala Gln Met Met Val Pro Asn Thr Thr Ile Arg Val Asp Arg Ala Met
 355 360 365
 Leu Arg Arg Leu Lys Thr Ala Glu Val Met Val Arg Thr Trp Pro Asn
 370 375 380
 Pro Val Ile Pro Lys Gln Tyr Phe Arg Ser His Gly Pro Gly Gly Ala
 385 390 395 400
 Ala Val Leu Gln Asp Pro Ala Asp Thr Ser Ser Ser Arg Met Ser Ser
 405 410 415

Arg Trp Arg Arg Trp Ser Val Ala Arg Arg Pro Ser Ala Ala Pro Pro
 420 425 430
 Cys Ala Ala Arg Ala Trp Arg Arg Ala Arg Thr Pro Arg Met Arg Val
 435 440 445
 Pro Ala Ala Thr Ser Trp Ala Gly Arg Trp Ala Ala Arg Val Gly Pro
 450 455 460
 Leu Gly Ala Pro Ala Arg Ala Cys Pro Cys Pro Ser Ser Arg Ala
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 Gly Trp Ile Pro Asp Val Gly Gly Glu
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<210> 19
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 <213> Chlamydomonas reinhardtii

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ccgtgtatac acatgctaaa	tatacttcgt taaatggag	ttcacccgccc aggcctgaac	180
atttgcgaa ccgctcctga	ggaagcagaa cgaatagcag	tgcatacacaaa tagcc atg	238
		Met	
		1	
<i>Af</i>			
gcg gac agg gta ctt gcc ctg gtc cat tac tat gct cgc gag ggc tat			286
Ala Asp Arg Val Leu Ala Leu Val His Tyr Tyr Ala Arg Glu Gly Tyr			
5	10	15	
ttt aga cat gtg cag acg gtg tgc aac gaa gtg ctc aag aag cgg ccg			334
Phe Arg His Val Gln Thr Val Cys Asn Glu Val Leu Lys Lys Arg Pro			
20	25	30	
gga gat ggc gta ctc aca ttc tgg cgt gcc tat gga ctg ctc atg gag			382
Gly Asp Gly Val Leu Thr Phe Trp Arg Ala Tyr Gly Leu Leu Met Glu			
35	40	45	
ggc aac acg gcg gac gcc atg cgt gac ctc tcc agc atc cag ggc aat			430
Gly Asn Thr Ala Asp Ala Met Arg Asp Leu Ser Ser Ile Gln Gly Asn			
50	55	60	65
tct gac ctt gag ctg gcg gtc gca gcc gcg caa cta ctg ggt cac gaa			478
Ser Asp Leu Glu Leu Ala Val Ala Ala Gln Leu Leu Gly His Glu			
70	75	80	
tcc gcc aag gtg ccc gac cac gat gcc atc att gac ctc caa gcc aag			526
Ser Ala Lys Val Pro Asp His Asp Ala Ile Ile Asp Leu Gln Ala Lys			
85	90	95	
ctg gag atc gag gag cgc acc gcc agc gac cag ccc tgc ctg cac ctg			574
Leu Glu Ile Glu Glu Arg Thr Ala Ser Asp Gln Pro Cys Leu His Leu			
100	105	110	

gcc tcc ttc tac ctg tat acc aag tcc aag gag cgc gcc cgcc ggt ctg Ala Ser Phe Tyr Leu Tyr Thr Lys Ser Lys Glu Arg Ala Arg Gly Leu 115 120 125	622
gtg gag cgc gtg ctg cgc aac cag ccc gac atg gtg ccg gcg cag gtt Val Glu Arg Val Leu Arg Asn Gln Pro Asp Met Val Pro Ala Gln Val 130 135 140 145	670
ctt ctg ggc tgg atc atc atc agc cag cag gac gac gag tac gac Leu Leu Gly Trp Ile Ile Ser Gln Gln Asp Asp Glu Tyr Asp 150 155 160	718
atg ctg ttt gac gag tcc gag ctg gac gac gcc ctc agc cac ttc gag Met Leu Phe Asp Glu Ser Glu Leu Asp Asp Ala Leu Ser His Phe Glu 165 170 175	766
cag gcg gtg gag cac gac cac aac gac ctg cag gcg ctg ctg ggc aaa Gln Ala Val Glu His Asp His Asn Asp Leu Gln Ala Leu Leu Gly Lys 180 185 190	814
gcc aag atc atg gag ctg aag aag cag ctg ggg ccc tgc ctg gac gtg Ala Lys Ile Met Glu Leu Lys Lys Gln Leu Gly Pro Cys Leu Asp Val 195 200 205	862
ctg acg gag atc aac gtg cgc ttc ggc tgg ttc gtg ccg gcg ctg gtg Leu Thr Glu Ile Asn Val Arg Phe Gly Trp Phe Val Pro Ala Leu Val 210 215 220 225	910
<i>OK</i> gaa aag acg cgc atg ctc atg atg ctg ggc gac tgg gag cag gtg acg Glu Lys Thr Arg Met Leu Met Met Leu Gly Asp Trp Glu Gln Val Thr 230 235 240	958
gag acg ctg cag cgg gtg ctt gcg gcg gac caa cag aac atc atg gcg Glu Thr Leu Gln Arg Val Leu Ala Ala Asp Gln Gln Asn Ile Met Ala 245 250 255	1006
cag gcc tgg aac tgc atg atc tcc ctc act cgc gag ggc aac aac aag Gln Ala Trp Asn Cys Met Ile Ser Leu Thr Arg Glu Gly Asn Asn Lys 260 265 270	1054
cag gcg gcc aag cag ctg cag gac ctg ttc agc tca atg aac cgc cag Gln Ala Ala Lys Gln Leu Gln Asp Leu Phe Ser Ser Met Asn Arg Gln 275 280 285	1102
gag ccc aag aac gcc gag ctc ttc cgc gtc gcc cgg ccc ttc ggc Glu Pro Lys Asn Ala Glu Leu Phe Phe Arg Val Ala Arg Pro Phe Gly 290 295 300 305	1150
cgc ctg gcc tgc agc gac ccc acg ctg ctg ggc atc acc tac ctc atg Arg Leu Ala Cys Ser Asp Pro Thr Leu Leu Gly Ile Thr Tyr Leu Met 310 315 320	1198
gcc gac cgc gcc gcg cag ctc agg ccg gag atg gcg gcc tac gtg gtg Ala Asp Arg Ala Ala Gln Leu Arg Pro Glu Met Ala Ala Tyr Val Val 325 330 335	1246

gag gca gct gct cag aag ctg atg atg gac gag acc acc aac gcc acg Glu Ala Ala Ala Gln Lys Leu Met Met Asp Glu Thr Thr Asn Ala Thr 340 345 350	1294
gag cgc ttc acg cag gcg cta cag ctg gac gag ctg aac ctg gag gcc Glu Arg Phe Thr Gln Ala Leu Gln Leu Asp Glu Leu Asn Leu Glu Ala 355 360 365	1342
aac gcg ggc gcg ctg gag gcg cag atc atg gcg ggc gag ctg gag gag Asn Ala Gly Ala Leu Glu Ala Gln Ile Met Ala Gly Glu Leu Glu Glu 370 375 380 385	1390
gcg gcg ggg cag atc atg ttc ctg gag gac atg ttc acc aac gcc gcg Ala Ala Gly Gln Ile Met Phe Leu Glu Asp Met Phe Thr Asn Ala Ala 390 395 400	1438
gcg gct ggc ggc ggc aag cgc aag ggc cgc ggc acc ggc gac atg gag Ala Ala Gly Gly Lys Arg Lys Gly Arg Gly Thr Gly Asp Met Asp 405 410 415	1486
gac gac ccc gat atg gcc gac ccc agt ctg ggc acc tcc tcc gac aac Asp Asp Pro Asp Met Ala Asp Pro Ser Leu Gly Thr Ser Ser Asp Asn 420 425 430	1534
ccc acg ctg ctc tac ctc aag ggt ctg ctg gcc tgg aag cag ggc atg Pro Thr Leu Leu Tyr Leu Lys Gly Leu Leu Ala Trp Lys Gln Gly Met 435 440 445	1582
ccg tcc gag ggc ctg ggt ctg ctg gag cgc tcc att gcc gcc ctg ttc Pro Ser Glu Gly Leu Gly Leu Leu Glu Arg Ser Ile Ala Ala Leu Phe 450 455 460 465	1630
tcc gcc gcc gcc gac ttc cac ggc ccc agc ctg gag ctg tac gcg gcg Ser Ala Ala Ala Asp Phe His Pro Ser Leu Glu Leu Tyr Ala Ala 470 475 480	1678
ctc aac ccg cgc cgc atc acc gca atg gtg cgg ctg ctg ctg cag agc Leu Asn Pro Ala Arg Ile Thr Ala Met Val Arg Leu Leu Leu Gln Ser 485 490 495	1726
atc ggc ggt gag ccg cgc gct ccc act gag gcg ccg tct ccg ctc atc Ile Gly Gly Glu Pro Arg Ala Pro Thr Glu Ala Pro Ser Pro Leu Ile 500 505 510	1774
agc aag gtc acc cgc gcg ctg gac ctg ctg aac aag cag gcg ccg gcg Ser Lys Val Thr Arg Ala Leu Asp Leu Leu Asn Lys Gln Ala Pro Ala 515 520 525	1822
ctg cag gag agc gcg ctg ctg cac gcg cgc gcg ctg tac ctg aac ggc Leu Gln Glu Ser Ala Leu Leu His Ala Arg Ala Leu Tyr Leu Asn Gly 530 535 540 545	1870
aac ctg gac ggc gcg ctg cgc aag gcg ggc gag atc ctg cgc atg aac Asn Leu Asp Gly Ala Leu Arg Lys Ala Gly Glu Ile Leu Arg Met Asn 550 555 560	1918

ccc gag gag agc tcc gcg cac ctg ctc atc tgt tcc gtg tac gtg gcg Pro Glu Glu Ser Ser Ala His Leu Leu Ile Cys Ser Val Tyr Val Ala 565 570 575	1966
cag gac aag ccc gag ctg gcc gtc agc gcg ctg gac cag gcc gtc agc Gln Asp Lys Pro Glu Leu Ala Val Ser Ala Leu Asp Gln Ala Val Ser 580 585 590	2014
agc aac ttc gcg atc cgc gag acg cct ctg tac cac gtg gtc cag gcc Ser Asn Phe Ala Ile Arg Glu Thr Pro Leu Tyr His Val Val Gln Ala 595 600 605	2062
aag gtg ctg gtg gcc aac aac aag ctg gac gac gcc aag cgc gtc ctg Lys Val Leu Val Ala Asn Asn Lys Leu Asp Asp Ala Lys Arg Val Leu 610 615 620 625	2110
gag tcc gcc atg aac ctg ccg ggc gtg cgc aca gcg ctc acc gtg cag Glu Ser Ala Met Asn Leu Pro Gly Val Arg Thr Ala Leu Thr Val Gln 630 635 640	2158
cag cgc gcg cga cta ggg cgc aag gtg gtc gag ccc acg ctg cac gag Gln Arg Ala Arg Leu Gly Arg Lys Val Val Glu Pro Thr Leu His Glu 645 650 655	2206
cgc gcc acc gtg tac ctg ctg gcg gac gtg ctg gcg agg cag tcc Arg Ala Thr Val Tyr Leu Leu Ala Asp Val Leu Ala Arg Gln Ser 660 665 670	2254
aag ata ccg gac gca cca gag gcc aag aag tac atc caa gac gcc atc Lys Ile Pro Asp Ala Pro Glu Ala Lys Lys Tyr Ile Gln Asp Ala Ile 675 680 685	2302
cgc gag ttc gag ggc acc agc gag gag gtg cgc gtc acg gtg gcg gac Arg Glu Phe Glu Gly Thr Ser Glu Glu Val Arg Val Thr Val Ala Asp 690 695 700 705	2350
tgc gag ctg gcc att gcg cgc ggc gac gtg gag ggc gcg ctc aag aag Cys Glu Leu Ala Ile Ala Arg Gly Asp Val Glu Gly Ala Leu Lys Lys 710 715 720	2398
ctg cgg cgc atc ccc aag gag tct ccg cac tac gtg aag gcg cgc atg Leu Arg Arg Ile Pro Lys Glu Ser Pro His Tyr Val Lys Ala Arg Met 725 730 735	2446
gcc atg gcc gac atc tac ctg cgc cac cgc aag gac aag gcc gcc tac Ala Met Ala Asp Ile Tyr Leu Arg His Arg Lys Asp Lys Ala Ala Tyr 740 745 750	2494
atc aag tgc tac atg gac ctg gtg gac cac acg ccc gac tac gac agc Ile Lys Cys Tyr Met Asp Leu Val Asp His Thr Pro Asp Tyr Asp Ser 755 760 765	2542
tac tgc atg ctg ggc gag gcg ttc atg cag atc cag gag ccg gag aag Tyr Cys Met Leu Gly Glu Ala Phe Met Gln Ile Gln Glu Pro Glu Lys 770 775 780 785	2590

gca gtg cgc gct
Ala Val Arg Ala

2602

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<212> PRT
<213> Chlamydomonas reinhardtii

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Tyr Phe Arg His Val Gln Thr Val Cys Asn Glu Val Leu Lys Lys Arg
20 25 30
Pro Gly Asp Gly Val Leu Thr Phe Trp Arg Ala Tyr Gly Leu Leu Met
35 40 45
Glu Gly Asn Thr Ala Asp Ala Met Arg Asp Leu Ser Ser Ile Gln Gly
50 55 60
Asn Ser Asp Leu Glu Leu Ala Val Ala Ala Gln Leu Leu Gly His
65 70 75 80
Glu Ser Ala Lys Val Pro Asp His Asp Ala Ile Ile Asp Leu Gln Ala
85 90 95
Lys Leu Glu Ile Glu Glu Arg Thr Ala Ser Asp Gln Pro Cys Leu His
100 105 110
Leu Ala Ser Phe Tyr Leu Tyr Thr Lys Ser Lys Glu Arg Ala Arg Gly
115 120 125
Leu Val Glu Arg Val Leu Arg Asn Gln Pro Asp Met Val Pro Ala Gln
130 135 140
Val Leu Leu Gly Trp Ile Ile Ile Ser Gln Gln Asp Asp Glu Tyr
145 150 155 160
Asp Met Leu Phe Asp Glu Ser Glu Leu Asp Asp Ala Leu Ser His Phe
165 170 175
Glu Gln Ala Val Glu His Asp His Asn Asp Leu Gln Ala Leu Leu Gly
180 185 190
Lys Ala Lys Ile Met Glu Leu Lys Lys Gln Leu Gly Pro Cys Leu Asp
195 200 205
Val Leu Thr Glu Ile Asn Val Arg Phe Gly Trp Phe Val Pro Ala Leu
210 215 220
Val Glu Lys Thr Arg Met Leu Met Met Leu Gly Asp Trp Glu Gln Val
225 230 235 240
Thr Glu Thr Leu Gln Arg Val Leu Ala Ala Asp Gln Gln Asn Ile Met
245 250 255
Ala Gln Ala Trp Asn Cys Met Ile Ser Leu Thr Arg Glu Gly Asn Asn
260 265 270
Lys Gln Ala Ala Lys Gln Leu Gln Asp Leu Phe Ser Ser Met Asn Arg
275 280 285
Gln Glu Pro Lys Asn Ala Glu Leu Phe Phe Arg Val Ala Arg Pro Phe
290 295 300
Gly Arg Leu Ala Cys Ser Asp Pro Thr Leu Leu Gly Ile Thr Tyr Leu
305 310 315 320
Met Ala Asp Arg Ala Ala Gln Leu Arg Pro Glu Met Ala Ala Tyr Val
325 330 335
Val Glu Ala Ala Ala Gln Lys Leu Met Met Asp Glu Thr Thr Asn Ala
340 345 350
Thr Glu Arg Phe Thr Gln Ala Leu Gln Leu Asp Glu Leu Asn Leu Glu
355 360 365

Ala Asn Ala Gly Ala Leu Glu Ala Gln Ile Met Ala Gly Glu Leu Glu
 370 375 380
 Glu Ala Ala Gly Gln Ile Met Phe Leu Glu Asp Met Phe Thr Asn Ala
 385 390 395 400
 Ala Ala Ala Gly Gly Lys Arg Lys Gly Arg Gly Thr Gly Asp Met
 405 410 415
 Asp Asp Asp Pro Asp Met Ala Asp Pro Ser Leu Gly Thr Ser Ser Asp
 420 425 430
 Asn Pro Thr Leu Leu Tyr Leu Lys Gly Leu Leu Ala Trp Lys Gln Gly
 435 440 445
 Met Pro Ser Glu Gly Leu Gly Leu Leu Glu Arg Ser Ile Ala Ala Leu
 450 455 460
 Phe Ser Ala Ala Ala Asp Phe His Gly Pro Ser Leu Glu Leu Tyr Ala
 465 470 475 480
 Ala Leu Asn Pro Ala Arg Ile Thr Ala Met Val Arg Leu Leu Gln
 485 490 495
 Ser Ile Gly Gly Glu Pro Arg Ala Pro Thr Glu Ala Pro Ser Pro Leu
 500 505 510
 Ile Ser Lys Val Thr Arg Ala Leu Asp Leu Leu Asn Lys Gln Ala Pro
 515 520 525
 Ala Leu Gln Glu Ser Ala Leu Leu His Ala Arg Ala Leu Tyr Leu Asn
 530 535 540
 Gly Asn Leu Asp Gly Ala Leu Arg Lys Ala Gly Glu Ile Leu Arg Met
 545 550 555 560
 Asn Pro Glu Glu Ser Ser Ala His Leu Leu Ile Cys Ser Val Tyr Val
 565 570 575
 Ala Gln Asp Lys Pro Glu Leu Ala Val Ser Ala Leu Asp Gln Ala Val
 580 585 590
 Ser Ser Asn Phe Ala Ile Arg Glu Thr Pro Leu Tyr His Val Val Gln
 595 600 605
 Ala Lys Val Leu Val Ala Asn Asn Lys Leu Asp Asp Ala Lys Arg Val
 610 615 620
 Leu Glu Ser Ala Met Asn Leu Pro Gly Val Arg Thr Ala Leu Thr Val
 625 630 635 640
 Gln Gln Arg Ala Arg Leu Gly Arg Lys Val Val Glu Pro Thr Leu His
 645 650 655
 Glu Arg Ala Thr Val Tyr Leu Leu Leu Ala Asp Val Leu Ala Arg Gln
 660 665 670
 Ser Lys Ile Pro Asp Ala Pro Glu Ala Lys Lys Tyr Ile Gln Asp Ala
 675 680 685
 Ile Arg Glu Phe Glu Gly Thr Ser Glu Glu Val Arg Val Thr Val Ala
 690 695 700
 Asp Cys Glu Leu Ala Ile Ala Arg Gly Asp Val Glu Gly Ala Leu Lys
 705 710 715 720
 Lys Leu Arg Arg Ile Pro Lys Glu Ser Pro His Tyr Val Lys Ala Arg
 725 730 735
 Met Ala Met Ala Asp Ile Tyr Leu Arg His Arg Lys Asp Lys Ala Ala
 740 745 750
 Tyr Ile Lys Cys Tyr Met Asp Leu Val Asp His Thr Pro Asp Tyr Asp
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<212> DNA

<213> Chlamydomonas reinhardtii

<220>

<221> CDS

<222> (1) ... (2295)

<400> 21

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aca gca gct gtc ggc tgg aat gtc tgg aat gaa ctg ttc act tgt agc	96
Thr Ala Ala Val Gly Trp Asn Val Trp Asn Glu Leu Phe Thr Cys Ser	
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gac gac cag act att cac aaa tgg aac atg ctg ggg gag cca gag cag	144
Asp Asp Gln Thr Ile His Lys Trp Asn Met Leu Gly Glu Pro Glu Gln	
35 40 45	

aag gtc agc act ctg gac gca tac ttc acg gat atg cac tgg tac ccc	192
Lys Val Ser Thr Leu Asp Ala Tyr Phe Thr Asp Met His Trp Tyr Pro	
50 55 60	

gtg agc tcg aag aag acg caa gca ggc ggg acg gac gta ttc gcg gtg	240
Val Ser Ser Lys Lys Thr Gln Ala Gly Gly Thr Asp Val Phe Ala Val	
65 70 75 80	

gcg tgc aca gac ggc tct gta aaa atc ctc acg cgc acg ggc cgc gtg	288
Ala Cys Thr Asp Gly Ser Val Lys Ile Leu Ser Arg Thr Gly Arg Val	
85 90 95	

gag aag tcc att gag ggg cac aag ggc gcg tgc atc tcg ctg cgc tgg	336
Glu Lys Ser Ile Glu Gly His Lys Gly Ala Cys Ile Ser Leu Arg Trp	
100 105 110	

agc tat gac ggg acg gca ctg gcg acg gcg ggc gag gac ggg tcg gta	384
Ser Tyr Asp Gly Thr Ala Leu Ala Thr Ala Gly Glu Asp Gly Ser Val	
115 120 125	

aag atc tgg tcg cgc aac ggc atg ctg cgc tcc acg cta gcg cag gcg	432
Lys Ile Trp Ser Arg Asn Gly Met Leu Arg Ser Thr Leu Ala Gln Ala	
130 135 140	

gac agc ccc gtg tac tcg att gtg tgg gcc tac gac tgc gac cag ctg	480
Asp Ser Pro Val Tyr Ser Ile Val Trp Ala Tyr Asp Cys Asp Gln Leu	
145 150 155 160	

tgc tac tgc acc ggc tcc aac gtg gtc atc aag tcg ctg tcc tcc aac	528
Cys Tyr Cys Thr Gly Ser Asn Val Val Ile Lys Ser Leu Ser Ser Asn	
165 170 175	

gcc aag cag aac gcg tgg aag gcg cac gac ggc gtg gtg ctc aag gtg	576
Ala Lys Gln Asn Ala Trp Lys Ala His Asp Gly Val Val Leu Lys Val	
180 185 190	

gac tgg agc ccc atc aac cac ctc atc atc aca ggc ggc gag gac tgc Asp Trp Ser Pro Ile Asn His Leu Ile Ile Thr Gly Gly Glu Asp Cys 195 200 205	624
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ctg ttc gac tac ccg gtc acg tcg gtg gcg tgg gcg ccc agc ggc gag Leu Phe Asp Tyr Pro Val Thr Ser Val Ala Trp Ala Pro Ser Gly Glu 225 230 235 240	720
ctg ttc gcg gtg ggc ggc ttc aac acg ctg cag ctg tgt gac cgc atg Leu Phe Ala Val Gly Gly Phe Asn Thr Leu Gln Leu Cys Asp Arg Met 245 250 255	768
ggc tgg gcc tac tcc aag atc cac ctc aac gac acg ggc agc atc atg Gly Trp Ala Tyr Ser Lys Ile His Leu Asn Asp Thr Gly Ser Ile Met 260 265 270	816
act ctg agc tgg acg gcg gac agc acg cag ctg gcg ggc ggc ggc Thr Leu Ser Trp Thr Ala Asp Ser Thr Gln Leu Ala Gly Gly Gly 275 280 285	864
agc ggc ggc gtg gtg ttc ggc cag gtg gtc gac ctg gcg ctg gag gac Ser Gly Gly Val Val Phe Gly Gln Val Val Asp Leu Ala Leu Glu Asp 290 295 300	912
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acg cag tgc cac gtg tac aac acc acc aac ctg ggc acg cgc cac atc Thr Gln Cys His Val Tyr Asn Thr Thr Asn Leu Gly Thr Pro His Ile 355 360 365	1104
ttt gac ctc aaa gac acg gtc acc ctg ctg cag gct gag cgg cac Phe Asp Leu Lys Asp Thr Val Thr Leu Leu Gln Ala Glu Arg His 370 375 380	1152
ttc ctg ctg ctg gac aac tcg gcg ggc atc cag atc tac acc tac gag Phe Leu Leu Leu Asp Asn Ser Ala Gly Ile Gln Ile Tyr Thr Tyr Glu 385 390 395 400	1200
ggc cgc cag atc tgc aac ccg cgc ttc cag ggc ctg cgc acc gag ctg Gly Arg Gln Ile Cys Asn Pro Arg Phe Gln Gly Leu Arg Thr Glu Leu 405 410 415	1248

ctg aac gcg cag atg atc acg ctg tcc aac gac acg ata gcg gtg ctg Leu Asn Ala Gln Met Ile Thr Leu Ser Asn Asp Thr Ile Ala Val Leu 420 425 430	1296
gac cag cag gcc agc ggc acc acc gtg cgc ttc ttc gac acg gcg cag Asp Gln Gln Ala Ser Gly Thr Thr Val Arg Phe Phe Asp Thr Ala Gln 435 440 445	1344
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atc gcg ctg agc cag gcc ggc acc atc aac gac cgc cag ctc atc gtc Ile Ala Leu Ser Gln Ala Gly Thr Ile Asn Asp Arg Gln Leu Ile Val 465 470 475 480	1440
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acc gcc atg ctg tcc gcc atg gtg gac cag cgc ctg tgt gtg tgg tac Thr Ala Met Leu Ser Ala Met Val Asp Gln Arg Leu Cys Val Trp Tyr 515 520 525	1584
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tac acc aag tcc gac tcg gac ttt ggc aag tcg gcc cag atc cag ctc Tyr Thr Lys Ser Asp Ser Asp Phe Gly Lys Ser Ala Gln Ile Gln Leu 545 550 555 560	1680
ttc gcc ggc aac cgc tgc ctg gtg cgc cgc tcc gac ggc gtg ctg gtc Phe Ala Gly Asn Arg Cys Leu Val Arg Arg Ser Asp Gly Val Leu Val 565 570 575	1728
tcc gcc gcc acc tcg ccc tac cct gcc gta ctg tac gac atg atc cgc Ser Ala Ala Thr Ser Pro Tyr Pro Ala Val Leu Tyr Asp Met Ile Arg 580 585 590	1776
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ccc acc atg tgg gcc acg ctg gcg gcg atg gcc atg gct aag gag Pro Thr Met Trp Ala Thr Leu Ala Ala Met Ala Met Ala Ala Lys Glu 610 615 620	1872
ctg aac acg gcg gag gtg gcg ttc gcg gcg att gac gag gtg gac aaa Leu Asn Thr Ala Glu Val Ala Phe Ala Ala Ile Asp Glu Val Asp Lys 625 630 635 640	1920

acg cac ttt gtg cgc aag gtg aag cag atc ccc acg gag gag ggc cgc Thr His Phe Val Arg Lys Val Lys Gln Ile Pro Thr Glu Glu Gly Arg 645 650 655	1968
aac gcc gag ctg gcg gtg tac cgg cgc aag ccc gag gag ggc gag tcc Asn Ala Glu Leu Ala Val Tyr Arg Arg Lys Pro Glu Glu Gly Glu Ser 660 665 670	2016
ata ctg ctg cag gcc ggc ctg gtc ttc cgc gcc atc aag ctg aac atc Ile Leu Leu Gln Ala Gly Leu Val Phe Arg Ala Ile Lys Leu Asn Ile 675 680 685	2064
aag ctg ttc aac tgg gag cgc gcg ctg sac ctg gcc acg cag cac aag Lys Leu Phe Asn Trp Glu Arg Ala Leu Xaa Leu Ala Thr Gln His Lys 690 695 700	2112
cag cac cag gac acg gtg ctg tgg tac cgc cag cag ttc ctc aag aac Gln His Gln Asp Thr Val Leu Trp Tyr Arg Gln Gln Phe Leu Lys Asn 705 710 715 720	2160
gcc aag ctc gcc gag tcc atc acg cgc ttc atg cag atg aac gag tcg Ala Lys Leu Ala Glu Ser Ile Thr Arg Phe Met Gln Met Asn Glu Ser 725 730 735	2208
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<210> 22
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 <212> PRT
 <213> Chlamydomonas reinhardtii

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 Asp Asp Gln Thr Ile His Lys Trp Asn Met Leu Gly Glu Pro Glu Gln
 35 40 45
 Lys Val Ser Thr Leu Asp Ala Tyr Phe Thr Asp Met His Trp Tyr Pro
 50 55 60
 Val Ser Ser Lys Lys Thr Gln Ala Gly Gly Thr Asp Val Phe Ala Val
 65 70 75 80
 Ala Cys Thr Asp Gly Ser Val Lys Ile Leu Ser Arg Thr Gly Arg Val
 85 90 95

Glu Lys Ser Ile Glu Gly His Lys Gly Ala Cys Ile Ser Leu Arg Trp
 100 105 110
 Ser Tyr Asp Gly Thr Ala Leu Ala Thr Ala Gly Glu Asp Gly Ser Val
 115 120 125
 Lys Ile Trp Ser Arg Asn Gly Met Leu Arg Ser Thr Leu Ala Gln Ala
 130 135 140
 Asp Ser Pro Val Tyr Ser Ile Val Trp Ala Tyr Asp Cys Asp Gln Leu
 145 150 155 160
 Cys Tyr Cys Thr Gly Ser Asn Val Val Ile Lys Ser Leu Ser Ser Asn
 165 170 175
 Ala Lys Gln Asn Ala Trp Lys Ala His Asp Gly Val Val Leu Lys Val
 180 185 190
 Asp Trp Ser Pro Ile Asn His Leu Ile Ile Thr Gly Gly Glu Asp Cys
 195 200 205
 Lys Tyr Lys Val Trp Asp Ser Phe Gly Arg Leu Leu Phe Gln Ser Gly
 210 215 220
 Leu Phe Asp Tyr Pro Val Thr Ser Val Ala Trp Ala Pro Ser Gly Glu
 225 230 235 240
 Leu Phe Ala Val Gly Phe Asn Thr Leu Gln Leu Cys Asp Arg Met
 245 250 255
 Gly Trp Ala Tyr Ser Lys Ile His Leu Asn Asp Thr Gly Ser Ile Met
 260 265 270
 Thr Leu Ser Trp Thr Ala Asp Ser Thr Gln Leu Ala Gly Gly Gly
 275 280 285
 Ser Gly Gly Val Val Phe Gly Gln Val Val Asp Leu Ala Leu Glu Asp
 290 295 300
 Gly Lys Met Gln Val Thr Val Val Asp Asp Met Arg Ile Val Val Asn
 305 310 315 320
 Asp Ile Leu Asn Glu Asn Ala Asp Glu Leu Pro Glu Phe Arg Asp Arg
 325 330 335
 Val Ile Lys Val Ser Leu Gly Tyr Gly Tyr Leu Ile Val Ala Thr Ala
 340 345 350
 Thr Gln Cys His Val Tyr Asn Thr Thr Asn Leu Gly Thr Pro His Ile
 355 360 365
 Phe Asp Leu Lys Asp Thr Val Thr Leu Leu Leu Gln Ala Glu Arg His
 370 375 380
 Phe Leu Leu Leu Asp Asn Ser Ala Gly Ile Gln Ile Tyr Thr Tyr Glu
 385 390 395 400
 Gly Arg Gln Ile Cys Asn Pro Arg Phe Gln Gly Leu Arg Thr Glu Leu
 405 410 415
 Leu Asn Ala Gln Met Ile Thr Leu Ser Asn Asp Thr Ile Ala Val Leu
 420 425 430
 Asp Gln Gln Ala Ser Gly Thr Thr Val Arg Phe Phe Asp Thr Ala Gln
 435 440 445
 Gly Arg Pro Val Gly Glu Pro Trp Gln His Thr Leu Glu Val Lys Glu
 450 455 460
 Ile Ala Leu Ser Gln Ala Gly Thr Ile Asn Asp Arg Gln Leu Ile Val
 465 470 475 480
 Ile Asp Arg Asn Arg Asp Leu Tyr Leu Leu Pro Val Met Lys Arg His
 485 490 495
 Val Ala Lys Leu Ala Ala Met Cys Asp Ser Ala Arg Trp His Asp Ser
 500 505 510
 Thr Ala Met Leu Ser Ala Met Val Asp Gln Arg Leu Cys Val Trp Tyr
 515 520 525
 Tyr Pro Ser Glu Val Tyr Val Asp Lys Asp Leu Leu Ala Lys Thr Arg
 530 535 540

Tyr Thr Lys Ser Asp Ser Asp Phe Gly Lys Ser Ala Gln Ile Gln Leu
 545 550 555 560
 Phe Ala Gly Asn Arg Cys Leu Val Arg Arg Ser Asp Gly Val Leu Val
 565 570 575
 Ser Ala Ala Thr Ser Pro Tyr Pro Ala Val Leu Tyr Asp Met Ile Arg
 580 585 590
 Lys Gln Gln Trp Asp Lys Ala Thr Arg Leu Cys Arg Phe Ile Lys Asp
 595 600 605
 Pro Thr Met Trp Ala Thr Leu Ala Ala Met Ala Met Ala Ala Lys Glu
 610 615 620
 Leu Asn Thr Ala Glu Val Ala Phe Ala Ala Ile Asp Glu Val Asp Lys
 625 630 635 640
 Thr His Phe Val Arg Lys Val Lys Gln Ile Pro Thr Glu Glu Gly Arg
 645 650 655
 Asn Ala Glu Leu Ala Val Tyr Arg Arg Lys Pro Glu Glu Gly Glu Ser
 660 665 670
 Ile Leu Leu Gln Ala Gly Leu Val Phe Arg Ala Ile Lys Leu Asn Ile
 675 680 685
 Lys Leu Phe Asn Trp Glu Arg Ala Leu Xaa Leu Ala Thr Gln His Lys
 690 695 700
 Gln His Gln Asp Thr Val Leu Trp Tyr Arg Gln Gln Phe Leu Lys Asn
 705 710 715 720
 Ala Lys Leu Ala Glu Ser Ile Thr Arg Phe Met Gln Met Asn Glu Ser
 725 730 735
 Val Val Val Asp Gln Ala Ala Val Lys Lys Lys Ile Glu Glu Glu Arg
 740 745 750
 Ile Lys Glu Ser Gln Arg Pro Gly Ala Lys Arg Tyr Val
 755 760 765

Af
 <210> 23
 <211> 132
 <212> PRT
 <213> Homo sapiens

<400> 23
 Met Ala Lys Asp Ile Leu Gly Glu Ala Gly Leu His Phe Asp Glu Leu
 1 5 10 15
 Asn Lys Leu Arg Val Leu Asp Pro Glu Val Thr Gln Gln Thr Ile Glu
 20 25 30
 Leu Lys Glu Glu Cys Lys Asp Phe Val Asp Lys Ile Gly Gln Phe Gln
 35 40 45
 Lys Ile Val Gly Gly Leu Ile Glu Leu Val Asp Gln Leu Ala Lys Glu
 50 55 60
 Ala Glu Asn Glu Lys Met Lys Ala Ile Gly Ala Arg Asn Leu Leu Lys
 65 70 75 80
 Ser Ile Ala Lys Gln Arg Glu Ala Gln Gln Gln Leu Gln Ala Leu
 85 90 95
 Ile Ala Glu Lys Lys Met Gln Leu Glu Arg Tyr Arg Val Glu Tyr Glu
 100 105 110
 Ala Leu Cys Lys Val Glu Ala Glu Gln Asn Glu Phe Ile Asp Gln Phe
 115 120 125
 Ile Phe Gln Lys
 130

<210> 24
 <211> 109

<212> PRT
<213> Homo sapiens

<220>
<221> VARIANT
<222> (1) ... (109)
<223> Xaa = any amino acid or absent

<400> 24
Gln Asp Ser Leu Gly Glu Ala Gly Leu Cys Phe Asp Glu Leu Ser Lys
1 5 10 15
Val Arg Asp Pro Glu Val Thr Xaa Gln Thr Arg Asp Pro Lys Glu Asp
20 25 30
Cys Met Asp Phe Val Gly Lys Ile Ser Pro Phe Gln Lys Glu Ile Val
35 40 45
Gly Gly Leu Ile Glu Pro Val Asp Gln Leu Ala Lys Ala Ala Glu Asn
50 55 60
Glu Lys Arg Lys Val Val Gly Ala Trp Asn Leu Leu Gln Phe Met Ala
65 70 75 80
Lys His Arg Glu Ala Gln Gln Gln Leu Leu Ala Gln Thr Ala Glu
85 90 95
Glu Lys Met Trp Leu Lys Arg Trp Trp Ile Glu Tyr Glu
100 105

af
<210> 25
<211> 76
<212> PRT
<213> Homo sapiens

<220>
<221> VARIANT
<222> (1) ... (76)
<223> Xaa = any amino acid or absent

<400> 25
Met Val Lys Asp Ile Leu Ala Glu Glu Gly Leu His Phe Asp Glu Leu
1 5 10 15
Asn Lys Leu Trp Val Leu Asp Ser Glu Val Thr Gln Gln Thr Thr Glu
20 25 30
Leu Lys Glu Glu Cys Lys Asn Phe Ala Asp Lys Thr Gly Gln Phe Gln
35 40 45
Lys Thr Val Gly Gly Leu Ile Glu Leu Val Asp Lys Leu Ala Lys Lys
50 55 60
Ala Xaa Asn Ala Lys Met Arg Ala Met Val Leu Arg
65 70 75

<210> 26
<211> 186
<212> PRT
<213> Homo sapiens

<400> 26
Met Val Lys Leu Ala Ala Lys Cys Ile Leu Ala Gly Asp Pro Ala Val
1 5 10 15
Gly Lys Thr Ala Leu Ala Gln Ile Phe Arg Ser Asp Gly Ala His Phe
20 25 30

Gln Lys Ser Tyr Thr Leu Thr Thr Gly Met Asp Leu Val Val Lys Thr
 35 40 45
 Val Pro Val Pro Asp Thr Gly Asp Ser Val Glu Leu Phe Ile Phe Asp
 50 55 60
 Ser Ala Gly Lys Glu Leu Phe Ser Glu Met Leu Asp Lys Leu Trp Glu
 65 70 75 80
 Ser Pro Asn Val Leu Cys Leu Val Tyr Asp Val Thr Asn Glu Glu Ser
 85 90 95
 Phe Asn Asn Cys Ser Lys Trp Leu Glu Lys Ala Arg Ser Gln Ala Pro
 100 105 110
 Gly Ile Ser Leu Pro Gly Val Leu Val Gly Asn Lys Thr Asp Leu Ala
 115 120 125
 Gly Arg Arg Ala Val Asp Ser Ala Glu Ala Arg Ala Trp Ala Leu Gly
 130 135 140
 Gln Gly Leu Glu Cys Phe Glu Thr Ser Val Lys Glu Met Glu Asn Phe
 145 150 155 160
 Glu Ala Pro Phe His Cys Leu Ala Lys Gln Phe His Gln Leu Tyr Arg
 165 170 175
 Glu Lys Val Glu Val Phe Arg Ala Leu Ala
 180 185

<210> 27

<211> 304

<212> PRT

<213> Homo sapiens

<400> 27

Met Ala Asp Asn Ser Ser Asp Glu Cys Glu Glu Glu Asn Asn Lys Glu
 1 5 10 15
 Lys Lys Lys Thr Ser Gln Leu Thr Pro Gln Arg Gly Phe Ser Glu Asn
 20 25 30
 Glu Asp Asp Asp Asp Asp Asp Asp Ser Ser Glu Thr Asp Ser Asp
 35 40 45
 Ser Asp Asp Asp Asp Glu Glu His Gly Ala Pro Leu Glu Gly Ala Tyr
 50 55 60
 Asp Pro Ala Asp Tyr Glu His Leu Pro Val Ser Ala Glu Ile Lys Glu
 65 70 75 80
 Leu Phe Gln Tyr Ile Ser Arg Tyr Thr Pro Gln Leu Ile Asp Leu Asp
 85 90 95
 His Lys Leu Lys Pro Phe Ile Pro Asp Phe Ile Pro Ala Val Gly Asp
 100 105 110
 Ile Asp Ala Phe Leu Lys Val Pro Arg Pro Asp Gly Lys Pro Asp Asn
 115 120 125
 Leu Gly Leu Leu Val Leu Asp Glu Pro Ser Thr Lys Gln Ser Asp Pro
 130 135 140
 Thr Val Leu Ser Leu Trp Leu Thr Glu Asn Ser Lys Gln His Asn Ile
 145 150 155 160
 Thr Gln His Met Lys Val Lys Ser Leu Glu Asp Ala Glu Lys Asn Pro
 165 170 175
 Lys Ala Ile Asp Thr Trp Ile Glu Ser Ile Ser Glu Leu His Arg Ser
 180 185 190
 Lys Pro Pro Ala Thr Val His Tyr Thr Arg Pro Met Pro Asp Ile Asp
 195 200 205
 Thr Leu Met Gln Glu Trp Ser Pro Glu Phe Glu Glu Leu Leu Gly Lys
 210 215 220
 Val Ser Leu Pro Thr Ala Glu Ile Asp Cys Ser Leu Ala Glu Tyr Ile
 225 230 235 240

Asp Met Ile Cys Ala Ile Leu Asp Ile Pro Val Tyr Lys Ser Arg Ile			
245	250	255	
Gln Ser Leu His Leu Leu Phe Ser Leu Tyr Ser Glu Phe Lys Asn Ser			
260	265	270	
Gln His Phe Lys Ala Leu Ala Glu Gly Lys Lys Ala Phe Thr Pro Ser			
275	280	285	
Ser Asn Ser Thr Ser Gln Ala Gly Asp Met Glu Thr Leu Thr Phe Ser			
290	295	300	

<210> 28
<211> 438
<212> PRT
<213> Homo sapiens

<400> 28

Met Glu Lys Glu Leu Arg Ser Thr Ile Leu Phe Asn Ala Tyr Lys Lys			
1	5	10	15
Glu Ile Phe Thr Thr Asn Asn Gly Tyr Lys Ser Met Gln Lys Lys Leu			
20	25	30	
Arg Ser Asn Trp Lys Ile Gln Ser Leu Lys Asp Glu Ile Thr Ser Glu			
35	40	45	
Lys Leu Asn Gly Val Lys Leu Trp Ile Thr Ala Gly Pro Arg Glu Lys			
50	55	60	
Phe Thr Ala Ala Glu Phe Glu Ile Leu Lys Lys Tyr Leu Asp Thr Gly			
65	70	75	80
Gly Asp Val Leu Val Met Leu Gly Glu Gly Glu Ser Arg Phe Asp			
85	90	95	
Thr Asn Ile Asn Phe Leu Leu Glu Glu Tyr Gly Ile Met Val Asn Asn			
100	105	110	
Asp Ala Val Val Arg Asn Val Tyr His Lys Tyr Phe His Pro Lys Glu			
115	120	125	
Ala Leu Val Ser Ser Gly Val Leu Asn Arg Glu Ile Ser Arg Ala Ala			
130	135	140	
Gly Lys Ala Val Leu Ala Ile Ile Asp Glu Glu Ser Ser Gly Asn Asn			
145	150	155	160
Ala Gln Ala Leu Thr Phe Val Tyr Pro Phe Gly Ala Thr Leu Ser Val			
165	170	175	
Met Lys Pro Ala Val Ala Val Leu Ser Thr Gly Ser Val Cys Phe Pro			
180	185	190	
Leu Asn Arg Pro Ile Leu Ala Phe Tyr His Ser Lys Asn Gln Gly Gly			
195	200	205	
Lys Leu Ala Val Leu Gly Ser Cys His Met Phe Ser Asp Gln Tyr Leu			
210	215	220	
Asp Lys Glu Glu Asn Ser Lys Ile Met Asp Val Val Val Phe Gln Trp			
225	230	235	240
Leu Thr Thr Gly Asp Ile His Leu Asn Gln Ile Asp Ala Glu Asp Pro			
245	250	255	
Glu Ile Ser Asp Tyr Met Met Leu Pro Tyr Thr Ala Thr Leu Ser Lys			
260	265	270	
Arg Asn Arg Glu Cys Leu Gln Glu Ser Asp Glu Ile Pro Arg Asp Phe			
275	280	285	
Thr Thr Leu Phe Asp Leu Ser Ile Phe Gln Leu Asp Thr Thr Ser Phe			
290	295	300	
His Ser Val Ile Glu Ala His Glu Gln Leu Asn Val Lys His Glu Pro			
305	310	315	320

Leu Gln Leu Ile Gln Pro Gln Phe Glu Thr Pro Leu Pro Thr Leu Gln
 325 330 335
 Pro Ala Val Phe Pro Pro Ser Phe Arg Glu Leu Pro Pro Pro Pro Leu
 340 345 350
 Glu Leu Phe Asp Leu Asp Glu Thr Phe Ser Ser Glu Lys Ala Arg Leu
 355 360 365
 Ala Gln Ile Thr Asn Lys Cys Thr Glu Glu Asp Leu Glu Phe Tyr Val
 370 375 380
 Arg Lys Cys Gly Asp Ile Leu Gly Val Thr Ser Lys Leu Pro Lys Asp
 385 390 395 400
 Gln Gln Asp Ala Lys His Ile Leu Glu His Val Phe Phe Gln Val Val
 405 410 415
 Glu Phe Lys Lys Leu Asn Gln Glu His Asp Ile Asp Thr Ser Glu Thr
 420 425 430
 Ala Phe Gln Asn Asn Phe
 435

<210> 29
 <211> 472
 <212> PRT
 <213> Caenorhabditis elegans

<400> 29

Met	Pro	Pro	Phe	Ser	Asp	Glu	Lys	Met	Thr	Asn	Arg	Ser	Ile	Gly	Arg
1								5		10					15
Lys	Val	Leu	Ile	Asp	Gln	Ser	Lys	Gln	Gln	Gln	Ile	Ser	Leu	Ile	Ser
								20		25					30
Gly	Phe	Arg	Gly	Val	Ala	Arg	His	Leu	Lys	Ser	Val	Leu	Thr	Val	Glu
								35		40					45
Ile	Asn	Thr	Glu	Pro	Ile	Asn	Leu	Asn	Gly	Leu	Glu	Asp	Val	Arg	Met
								50		55					60
Leu	Ile	Ile	Pro	Gln	Pro	Lys	Thr	Ser	Phe	Gly	Thr	Gly	Glu	Ile	Glu
								65		70					80
Ala	Ile	Trp	Lys	Phe	Val	Glu	Glu	Gly	Gly	Ser	Leu	Met	Ile	Leu	Ser
								85		90					95
Gly	Glu	Gly	Glu	Arg	Gln	Ser	Leu	Asn	Glu	Met	Ile	Ala	Lys	Tyr	
								100		105					110
Gly	Ile	Thr	Val	Asn	Lys	Asp	Ser	Val	Ile	Arg	Thr	Val	Phe	Leu	Lys
								115		120					125
Tyr	Phe	Asp	Pro	Lys	Glu	Ala	Leu	Val	Ala	Asn	Gly	Val	Ile	Asn	Arg
								130		135					140
Ala	Ile	Ala	Val	Ala	Ala	Lys	Lys	Asn	Val	Ser	Thr	Glu	Gln	Lys	His
								145		150					160
Asn	Ser	Gln	Ala	Leu	Ser	Phe	Ile	Tyr	Pro	Tyr	Gly	Cys	Thr	Leu	Asp
								165		170					175
Val	Asn	Asn	Arg	Met	Ser	Asn	Val	Val	Leu	Ser	Ser	Gly	Ser	Thr	Ser
								180		185					190
Phe	Pro	Thr	Ser	Arg	Pro	Val	Ala	Ala	Phe	His	Glu	Thr	Lys	Leu	Asn
								195		200					205
Glu	Met	Lys	Lys	Lys	Gly	Arg	Val	Cys	Val	Val	Gly	Ser	Val	Ser	Met
								210		215					220
Phe	His	Asp	Thr	Tyr	Ile	Asp	Lys	Glu	Glu	Asn	Gly	Lys	Ile	Phe	Asp
								225		230					240
Thr	Phe	Val	Glu	Phe	Leu	Val	Asn	Gly	Leu	Glu	Leu	Asn	Thr	Ile	Asp
								245		250					255
Ala	Ala	Glu	Pro	Glu	Ile	Asn	Asp	Tyr	Thr	Asn	Ile	Pro	Asp	His	Ile
								260		265					270

His Met Ser Gln Gln Ile Lys Val Cys Met Tyr Glu Gly Glu Leu Asp
 275 280 285
 Gln Ala Ile Ser Ser Asp Phe Met Lys Ile Met Asp Thr Ser Leu His
 290 295 300
 Ser Phe Asn Leu Lys His Trp Pro Met Thr Ile Arg Leu Tyr Glu Ala
 305 310 315 320
 Leu Asn Leu Ser Pro Pro Leu Thr Leu Val Glu Pro Gln Phe Glu
 325 330 335
 Leu Pro Met Pro Pro Phe Gln Pro Ala Val Phe Pro Pro Thr Phe Gln
 340 345 350
 Glu Leu Pro Met Pro Pro Leu Glu Leu Phe Asp Leu Asp Glu Gln Phe
 355 360 365
 Ser Ser Pro Glu Ile Gln Leu Ser Gln Leu Ala Asn Arg Ser Glu Glu
 370 375 380
 Glu Asp Leu Ile Phe Phe Ile Glu Lys Ala Gly Glu Ile Thr Gly Ile
 385 390 395 400
 Ser Ala Glu Leu Thr Arg Ser Glu Arg Thr Pro Lys Lys Ile Ile Glu
 405 410 415
 Leu Ala Val Ser Lys Leu Met Leu Phe Lys Arg Ser Met Met Asp Gly
 420 425 430
 Glu Leu Glu Val Ala Ser Ala Phe Asp Ile Gly Glu His Asp Ala His
 435 440 445
 His Gln Ser Phe Asn Gln Gly Glu Glu Met Asp Glu Gln Leu Phe Ser
 450 455 460
 Asp Ile Asp Glu Phe Asp Asp Leu
 465 470

A
 <210> 30
 <211> 429
 <212> PRT
 <213> Homo sapiens

<400> 30
 Met Thr Ala Ala Leu Ala Val Val Thr Thr Ser Gly Leu Glu Asp Gly
 1 5 10 15
 Val Pro Arg Ser Arg Gly Glu Gly Thr Gly Glu Val Val Leu Glu Arg
 20 25 30
 Gly Pro Gly Ala Ala Tyr His Met Phe Val Val Met Glu Asp Leu Val
 35 40 45
 Glu Lys Leu Lys Leu Leu Arg Tyr Glu Glu Glu Phe Leu Arg Lys Ser
 50 55 60
 Asn Leu Lys Ala Pro Ser Arg His Tyr Phe Ala Leu Pro Thr Asn Pro
 65 70 75 80
 Gly Glu Gln Phe Tyr Met Phe Cys Thr Leu Ala Ala Trp Leu Ile Asn
 85 90 95
 Lys Ala Gly Arg Pro Phe Glu Gln Pro Gln Glu Tyr Asp Asp Pro Asn
 100 105 110
 Ala Thr Ile Ser Asn Ile Leu Ser Glu Leu Arg Ser Phe Gly Arg Thr
 115 120 125
 Ala Asp Phe Pro Pro Ser Lys Leu Lys Ser Gly Tyr Gly Glu His Val
 130 135 140
 Cys Tyr Val Leu Asp Cys Phe Ala Glu Glu Ala Leu Lys Tyr Ile Gly
 145 150 155 160
 Phe Thr Trp Lys Arg Pro Ile Tyr Pro Val Glu Glu Leu Glu Glu
 165 170 175
 Ser Val Ala Glu Asp Asp Ala Glu Leu Thr Leu Asn Lys Val Asp Glu
 180 185 190

Glu Phe Val Glu Glu Glu Thr Asp Asn Glu Glu Asn Phe Ile Asp Leu
 195 200 205
 Asn Val Leu Lys Ala Gln Thr Tyr His Leu Asp Met Asn Glu Thr Ala
 210 215 220
 Lys Gln Glu Asp Ile Leu Glu Ser Thr Thr Asp Ala Ala Glu Trp Ser
 225 230 235 240
 Leu Glu Val Glu Arg Val Leu Pro Gln Leu Lys Val Thr Ile Arg Thr
 245 250 255
 Asp Asn Lys Asp Trp Arg Ile His Val Asp Gln Met His Gln His Arg
 260 265 270
 Ser Gly Ile Glu Ser Ala Leu Lys Glu Thr Lys Gly Phe Leu Asp Lys
 275 280 285
 Leu His Asn Glu Ile Thr Arg Thr Leu Glu Lys Ile Ser Ser Arg Glu
 290 295 300
 Lys Tyr Ile Asn Asn Gln Leu Glu Asn Leu Val Gln Glu Tyr Arg Ala
 305 310 315 320
 Ala Gln Ala Gln Leu Ser Glu Ala Lys Glu Arg Tyr Gln Gln Gly Asn
 325 330 335
 Gly Gly Val Thr Glu Arg Thr Arg Leu Leu Ser Glu Val Met Glu Glu
 340 345 350
 Leu Glu Lys Val Lys Gln Glu Met Glu Glu Lys Gly Ser Ser Met Thr
 355 360 365
 Asp Gly Ala Pro Leu Val Lys Ile Lys Gln Ser Leu Thr Lys Leu Lys
 370 375 380
 Gln Glu Thr Val Glu Met Asp Ile Arg Ile Gly Ile Val Glu His Thr
 385 390 395 400
 Leu Leu Gln Ser Lys Leu Lys Glu Lys Ser Asn Met Thr Arg Asn Met
 405 410 415
 His Ala Thr Val Ile Pro Glu Pro Ala Thr Gly Phe Tyr
 420 425

Off
 <210> 31
 <211> 141
 <212> PRT
 <213> Homo sapiens

<400> 31
 Asp Gln Arg Ile His Val Asp Gln Met Tyr Gln His Lys Ser Gly Ile
 1 5 10 15
 Glu Ser Ser Leu Lys Glu Ser Lys Arg Phe Phe Asp Lys Leu His Asn
 20 25 30
 Glu Ile Ser Lys Thr Leu Glu Lys Ile Ser His Cys Glu Lys Tyr Ile
 35 40 45
 Asn His Gln Leu Glu His Arg Val Gln Glu Tyr Pro Ala Ala Gln Thr
 50 55 60
 Gln Leu Ser Asp Val Arg Ser Gln Gln Gly Ser Gly Gly Val Ile Glu
 65 70 75 80
 Arg Thr Arg Leu Leu Ser Glu Ala Thr Glu Asp Thr Glu His Val Lys
 85 90 95
 Leu Glu Met Glu Glu Lys Cys Ser Ser Met Thr Asp Gly Asp Ser Leu
 100 105 110
 Val Lys Ile Lys Gln Ser Leu Thr Lys Leu Lys Gln Glu Thr Val Gln
 115 120 125
 Met Asp Ile Arg Ile Gly Val Val Glu His Thr Leu Leu
 130 135 140

<210> 32
<211> 325
<212> PRT
<213> *Caenorhabditis elegans*

<400> 32

Met	Leu	His	His	Ile	Lys	Ser	Leu	Lys	Ser	Val	Leu	Ser	Arg	Gly	Gln
1				5				10					15		
Glu	Gly	Arg	Phe	Gly	Glu	Lys	Arg	His	Ser	Asn	Thr	Thr	Phe	Ile	Thr
				20				25					30		
Gly	Ile	Ala	Thr	Asp	Phe	Thr	Ala	Ala	Lys	Leu	Lys	Ser	Gly	Ala	Gly
	35				40				45						
Glu	Asn	Val	Ile	Phe	Ile	Leu	Asn	Ser	Leu	Ala	Asp	Ala	Ser	Leu	Val
	50				55				60						
His	Val	Gly	Phe	Gln	Trp	Gln	Lys	Met	Ile	Pro	Pro	Lys	Glu	Glu	Asp
	65				70				75				80		
Glu	Asp	Thr	Ala	Val	Asp	Glu	Gln	Asp	Glu	Asp	Asp	Asp	Asn	Asp	Asp
					85				90				95		
Ile	Val	Glu	Glu	Pro	Met	Asn	Phe	Leu	Asp	Asp	Asp	Asp	Asp	Asp	Asn
		100				105				110					
Val	Ile	Glu	Ile	Asp	Leu	Lys	Ala	Gln	Gly	Leu	Ala	Thr	Glu	Ser	Lys
	115					120				125					
Asn	Pro	Leu	Gln	Ser	Val	Leu	Gln	Ser	Asn	Thr	Asp	Ala	Ile	Thr	Trp
	130					135				140					
Lys	Gln	Glu	Val	Glu	Arg	Val	Ala	Pro	Gln	Leu	Lys	Ile	Thr	Leu	Lys
	145					150				155				160	
Gln	Asp	Ala	Lys	Asp	Trp	Arg	Leu	His	Leu	Glu	Gln	Met	Asn	Ser	Met
		165					170				175				
His	Lys	Asn	Val	Glu	Gln	Lys	Val	Gly	Asn	Val	Gly	Pro	Tyr	Leu	Asp
		180					185				190				
Asn	Met	Ser	Lys	Asp	Ile	Ala	Lys	Ala	Leu	Glu	Arg	Ile	Ala	Ser	Arg
	195					200				205					
Glu	Lys	Ser	Leu	Asn	Ser	Gln	Leu	Ala	Ser	Met	Met	Ser	Lys	Phe	Arg
	210					215				220					
Arg	Ala	Thr	Asp	Thr	Arg	Ala	Glu	Leu	Arg	Glu	Lys	Tyr	Lys	Ala	Ala
	225					230				235				240	
Ser	Val	Gly	Val	Ser	Ser	Arg	Thr	Glu	Thr	Leu	Asp	Arg	Ile	Ser	Asp
		245					250				255				
Asp	Ile	Glu	Gln	Leu	Lys	Gln	Gln	Ile	Glu	Glu	Gln	Gly	Ala	Lys	Ser
		260					265				270				
Ser	Asp	Gly	Ala	Pro	Leu	Val	Lys	Ile	Lys	Gln	Ala	Val	Ser	Lys	Leu
	275					280				285					
Glu	Glu	Glu	Leu	Gln	Thr	Met	Asn	Val	Gln	Ile	Gly	Val	Phe	Glu	Gln
	290				295				300						
Ser	Ile	Leu	Asn	Thr	Tyr	Leu	Arg	Asp	His	Phe	Asn	Phe	Ser	Ala	Asn
	305					310				315				320	
Leu	Leu	Asn	Ile	Met											
		325													

<210> 33
<211> 435
<212> PRT
<213> *Homo sapiens*

<400> 33

Met	Glu	Glu	Val	Met	Asn	Gly	Tyr	Asn	Met	Leu	Lys	Ala	Gln	Asn	Asp
1				5					10				15		

Arg Glu Thr Gln Ser Leu Asp Val Ile Phe Thr Glu Arg Gln Ala Lys
 20 25 30
 Glu Lys Gln Ile Arg Ser Val Glu Glu Glu Ile Glu Gln Glu Lys Gln
 35 40 45
 Ala Thr Asp Asp Ile Ile Lys Asn Met Ser Leu Glu Asn Gln Val Lys
 50 55 60
 Tyr Leu Glu Met Lys Thr Thr Asn Glu Lys Leu Leu Gln Glu Leu Asp
 65 70 75 80
 Thr Leu Gln Gln Leu Asp Ser Gln Asn Met Lys Lys Glu Ser Leu
 85 90 95
 Glu Ala Glu Ile Ala His Ser Gln Val Lys Gln Glu Ala Val Leu Leu
 100 105 110
 His Glu Lys Leu Tyr Glu Leu Glu Ser His Arg Asp Gln Met Ile Ala
 115 120 125
 Glu Asp Lys Ser Ile Gly Ser Pro Met Glu Glu Arg Glu Lys Leu Leu
 130 135 140
 Lys Gln Ile Lys Asp Asp Asn Gln Glu Ile Ala Ser Met Glu Arg Gln
 145 150 155 160
 Leu Thr Asp Thr Lys Glu Lys Ile Asn Gln Phe Ile Glu Glu Ile Arg
 165 170 175
 Gln Leu Asp Met Asp Leu Glu Glu His Gln Gly Glu Met Asn Gln Lys
 180 185 190
 Tyr Lys Glu Leu Lys Lys Arg Glu Glu His Met Asp Thr Phe Ile Glu
 195 200 205
 Thr Phe Glu Glu Thr Lys Asn Gln Glu Leu Lys Arg Lys Ala Gln Ile
 210 215 220
 Glu Ala Asn Ile Val Ala Leu Leu Glu His Cys Ser Arg Asn Ile Asn
 225 230 235 240
 Arg Ile Glu Gln Ile Ser Ser Ile Thr Asn Gln Glu Leu Lys Met Met
 245 250 255
 Gln Asp Asp Leu Asn Phe Lys Ser Thr Glu Val Gln Lys Ser Gln Ser
 260 265 270
 Thr Ala Gln Asn Leu Thr Ser Asp Ile Gln Arg Leu Gln Leu Asp Leu
 275 280 285
 Gln Lys Met Glu Leu Leu Glu Ser Lys Met Thr Glu Glu Gln His Ser
 290 295 300
 Leu Lys Ser Lys Ile Lys Gln Met Thr Thr Asp Leu Glu Ile Tyr Asn
 305 310 315 320
 Asp Leu Pro Ala Leu Lys Ser Ser Gly Glu Glu Lys Ile Lys Lys Leu
 325 330 335
 His Gln Glu Arg Met Ile Leu Ser Thr His Arg Asn Ala Phe Lys Lys
 340 345 350
 Ile Met Glu Lys Gln Asn Ile Glu Tyr Glu Ala Leu Lys Thr Gln Leu
 355 360 365
 Gln Glu Asn Glu Thr His Ser Gln Leu Thr Asn Leu Glu Arg Lys Trp
 370 375 380
 Gln His Leu Glu Gln Asn Asn Phe Ala Met Lys Glu Phe Ile Ala Thr
 385 390 395 400
 Lys Ser Gln Glu Ser Asp Tyr Gln Pro Ile Lys Lys Asn Val Thr Lys
 405 410 415
 Gln Ile Ala Glu Tyr Asn Lys Thr Ile Val Asp Ala Leu His Ser Thr
 420 425 430
 Ser Gly Asn
 435

<210> 34

<211> 824

<212> PRT
<213> Homo sapiens

<400> 34

Met Met Gln Asn Val His Leu Ala Pro Glu Thr Asp Glu Asp Asp Leu
1 5 10 15
Tyr Ser Gly Tyr Asn Asp Tyr Asn Pro Ile Tyr Asp Ile Glu Glu Leu
20 25 30
Glu Asn Asp Ala Ala Phe Gln Gln Ala Val Arg Thr Ser His Gly Arg
35 40 45
Arg Pro Pro Ile Thr Ala Lys Ile Ser Ser Thr Ala Val Thr Arg Pro
50 55 60
Ile Ala Thr Gly Tyr Gly Ser Lys Thr Ser Leu Ala Ser Ser Ile Gly
65 70 75 80
Arg Pro Met Thr Gly Ala Ile Gln Asp Gly Val Thr Arg Pro Met Thr
85 90 95
Ala Val Arg Ala Ala Gly Phe Thr Lys Ala Ala Leu Arg Gly Ser Ala
100 105 110
Phe Asp Pro Leu Ser Gln Ser Arg Gly Pro Ala Ser Pro Leu Glu Ala
115 120 125
Lys Lys Lys Asp Ser Pro Glu Glu Lys Ile Lys Gln Leu Glu Lys Glu
130 135 140
Val Asn Glu Leu Val Glu Glu Ser Cys Ile Ala Asn Ser Cys Gly Asp
145 150 155 160
Leu Lys Leu Ala Leu Glu Lys Ala Lys Asp Ala Gly Arg Lys Glu Arg
165 170 175
Val Leu Val Arg Gln Arg Glu Gln Val Thr Thr Pro Glu Asn Ile Asn
180 185 190
Leu Asp Leu Thr Tyr Ser Val Leu Ser Asn Leu Ala Ser Gln Tyr Ser
195 200 205
Val Asn Glu Met Tyr Ala Glu Ala Leu Asn Thr Tyr Gln Val Ile Val
210 215 220
Lys Asn Lys Met Phe Ser Asn Ala Gly Ile Leu Lys Met Asn Met Gly
225 230 235 240
Asn Ile Tyr Leu Lys Gln Arg Asn Tyr Ser Lys Ala Ile Lys Phe Tyr
245 250 255
Arg Met Ala Leu Asp Gln Val Pro Ser Val Asn Lys Gln Met Arg Ile
260 265 270
Lys Ile Met Gln Asn Ile Gly Val Thr Phe Ile Gln Ala Gly Gln Tyr
275 280 285
Ser Asp Ala Ile Asn Ser Tyr Glu His Ile Met Ser Met Ala Pro Asn
290 295 300
Leu Lys Ala Gly Tyr Asn Leu Thr Ile Cys Tyr Phe Ala Ile Gly Asp
305 310 315 320
Arg Glu Lys Met Lys Lys Ala Phe Gln Lys Leu Ile Thr Val Pro Leu
325 330 335
Glu Ile Asp Glu Asp Lys Tyr Ile Ser Pro Ser Asp Asp Pro His Thr
340 345 350
Asn Leu Val Thr Glu Ala Ile Lys Asn Asp His Leu Arg Gln Met Glu
355 360 365
Arg Glu Arg Lys Ala Met Ala Glu Lys Tyr Ile Thr Thr Ser Ala Lys
370 375 380
Leu Ile Ala Pro Val Ile Glu Thr Ser Phe Ala Ala Gly Cys Asp Trp
385 390 395 400
Cys Val Glu Val Val Lys Ala Ser Gln Tyr Val Glu Leu Ala Asn Asp
405 410 415

Leu Glu Ile Asn Lys Ala Val Thr Tyr Leu Arg Gln Lys Asp Tyr Asn
 420 425 430
 Gln Ala Val Glu Ile Leu Lys Val Leu Glu Lys Lys Asp Asn Arg Val
 435 440 445
 Lys Ser Ala Ala Ala Thr Asn Leu Ser Ala Leu Tyr Tyr Met Gly Lys
 450 455 460
 Asp Phe Ala Gln Ala Ser Ser Tyr Ala Asp Ile Ala Val Asn Ser Asp
 465 470 475 480
 Arg Tyr Asn Pro Ala Ala Leu Thr Asn Lys Gly Asn Thr Val Phe Ala
 485 490 495
 Asn Gly Asp Tyr Glu Lys Ala Ala Glu Phe Tyr Lys Glu Ala Leu Arg
 500 505 510
 Asn Asp Ser Ser Cys Thr Glu Ala Leu Tyr Asn Ile Gly Leu Thr Tyr
 515 520 525
 Glu Lys Leu Asn Arg Leu Asp Glu Ala Leu Asp Cys Phe Leu Lys Leu
 530 535 540
 His Ala Ile Leu Arg Asn Ser Ala Glu Val Leu Tyr Gln Ile Ala Asn
 545 550 555 560
 Ile Tyr Glu Leu Met Glu Asn Pro Ser Gln Ala Ile Glu Trp Leu Met
 565 570 575
 Gln Val Val Ser Val Ile Pro Thr Asp Pro Gln Val Leu Ser Lys Leu
 580 585 590
 Gly Glu Leu Tyr Asp Arg Glu Gly Asp Lys Ser Gln Ala Phe Gln Tyr
 595 600 605
 Tyr Tyr Glu Ser Tyr Arg Tyr Phe Pro Cys Asn Ile Glu Val Ile Glu
 610 615 620
 Trp Leu Gly Ala Tyr Tyr Ile Asp Thr Gln Phe Trp Glu Lys Ala Ile
 625 630 635 640
 Gln Tyr Phe Glu Arg Ala Ser Leu Ile Gln Pro Thr Gln Val Lys Trp
 645 650 655
 Gln Leu Met Val Ala Ser Cys Phe Arg Arg Ser Gly Asn Tyr Gln Lys
 660 665 670
 Ala Leu Asp Thr Tyr Lys Asp Thr His Arg Lys Phe Pro Glu Asn Val
 675 680 685
 Glu Cys Leu Arg Phe Leu Val Arg Leu Cys Thr Asp Leu Gly Leu Lys
 690 695 700
 Asp Ala Gln Glu Tyr Ala Arg Lys Leu Lys Arg Leu Glu Lys Met Lys
 705 710 715 720
 Glu Ile Arg Glu Gln Arg Ile Lys Ser Gly Arg Asp Gly Ser Gly Gly
 725 730 735
 Ser Arg Gly Lys Arg Glu Gly Ser Ala Ser Gly Asp Ser Gly Gln Asn
 740 745 750
 Tyr Ser Ala Ser Ser Lys Gly Glu Arg Leu Ser Ala Arg Leu Arg Ala
 755 760 765
 Leu Pro Gly Thr Asn Glu Pro Tyr Glu Ser Ser Ser Asn Lys Glu Ile
 770 775 780
 Asp Ala Ser Tyr Val Asp Pro Leu Gly Pro Gln Ile Glu Arg Pro Lys
 785 790 795 800
 Thr Ala Ala Lys Lys Arg Ile Asp Glu Asp Asp Phe Ala Asp Glu Glu
 805 810 815
 Leu Gly Asp Asp Leu Leu Pro Glu
 820

<210> 35

<211> 820

<212> PRT

<213> Caenorhabditis elegans

<400> 35

Met Ala Asn Ser Thr Phe Arg Glu Asp Asp Asp Asp Phe Tyr Gly Gly
 1 5 10 15
 Phe Asp Ser Tyr Asp Lys Ala Tyr Asp Ile Gln Asn Ile Thr Gln Asn
 20 25 30
 Pro Gln Phe Gln Gln Ala Val Ala Arg Ser Ser His Gly Arg Arg Pro
 35 40 45
 Thr Ala Ser Gln Met Gly Phe Arg Asp Ala Ser Ser Ser Tyr Gly Lys
 50 55 60
 Pro Pro Gly Thr Met Met Gly Asn Gln Ser Arg Met Gly Gly Arg Thr
 65 70 75 80
 Ala Met Ala Asn Asn Asn Glu Pro Ala Arg Pro Met Thr Ala Val Arg
 85 90 95
 Gly Ala Gly Tyr Thr Ser Phe Ala Asn Lys Val Gln Ala Ala Glu Arg
 100 105 110
 Pro Leu Ser Thr Glu Asn Ser Gly Glu Asn Gly Glu Glu Lys Cys Arg
 115 120 125
 Gln Met Glu Asn Lys Val Met Glu Met Leu Arg Glu Ser Met Leu Ala
 130 135 140
 Ser Glu Lys Lys Lys Phe Lys Glu Ala Leu Asp Lys Ala Lys Glu Ala
 145 150 155 160
 Gly Arg Arg Glu Arg Ala Val Val Lys His Arg Glu Gln Gln Gly Leu
 165 170 175
 Val Glu Met Met Asn Leu Asp Leu Thr Phe Thr Val Leu Phe Asn Leu
 180 185 190
 Ala Gln Gln Tyr Glu Ala Asn Asp Met Thr Asn Glu Ala Leu Asn Thr
 195 200 205
 Tyr Glu Ile Ile Val Arg Asn Lys Met Phe Pro Asn Ser Gly Arg Leu
 210 215 220
 Lys Val Asn Ile Gly Asn Ile His Phe Arg Lys Arg Glu Phe Thr Lys
 225 230 235 240
 Ala Leu Lys Tyr Tyr Arg Met Ala Leu Asp Gln Val Pro Ser Ile Gln
 245 250 255
 Lys Asp Thr Arg Ile Lys Ile Leu Asn Asn Ile Gly Val Thr Phe Val
 260 265 270
 Arg Met Gly Ser Tyr Asp Asp Ala Ile Ser Thr Phe Asp His Cys Val
 275 280 285
 Glu Glu Asn Pro Asn Phe Ile Thr Ala Leu Asn Leu Ile Leu Val Ala
 290 295 300
 Phe Cys Ile Gln Asp Ala Glu Lys Met Arg Glu Ala Phe Val Lys Met
 305 310 315 320
 Ile Asp Ile Pro Gly Phe Pro Asp Asp Tyr Met Lys Glu Lys Asp
 325 330 335
 Asp Asp Asp Val Leu Leu Asn Gln Thr Leu Asn Ser Asp Met Leu Lys
 340 345 350
 Asn Trp Glu Lys Arg Asn Lys Ser Asp Ala Glu Lys Ala Ile Ile Thr
 355 360 365
 Ala Val Lys Ile Ile Ser Pro Val Ile Ala Pro Asp Tyr Ala Ile Gly
 370 375 380
 Tyr Glu Trp Cys Leu Glu Ser Leu Lys Gln Ser Val His Ala Pro Leu
 385 390 395 400
 Ala Ile Glu Leu Glu Met Thr Lys Ala Gly Glu Leu Met Lys Asn Gly
 405 410 415
 Asp Ile Glu Gly Ala Ile Glu Val Leu Lys Val Phe Asn Ser Gln Asp
 420 425 430

Ser Lys Thr Ala Ser Ala Ala Asn Asn Leu Cys Met Leu Arg Phe
 435 440 445
 Leu Gln Gly Gly Arg Arg Leu Val Asp Ala Gln Gln Tyr Ala Asp Gln
 450 455 460
 Ala Leu Ser Ile Asp Arg Tyr Asn Ala His Ala Gln Val Asn Gln Gly
 465 470 475 480
 Asn Ile Ala Tyr Met Asn Gly Asp Leu Asp Lys Ala Leu Asn Asn Tyr
 485 490 495
 Arg Glu Ala Leu Asn Asn Asp Ala Ser Cys Val Gln Ala Leu Phe Asn
 500 505 510
 Ile Gly Leu Thr Ala Lys Ala Gln Gly Asn Leu Glu Gln Ala Leu Glu
 515 520 525
 Phe Phe Tyr Lys Leu His Gly Ile Leu Leu Asn Asn Val Gln Val Leu
 530 535 540
 Val Gln Leu Ala Ser Ile Tyr Glu Ser Leu Glu Asp Ser Ala Gln Ala
 545 550 555 560
 Ile Glu Leu Tyr Ser Gln Ala Asn Ser Leu Val Pro Asn Asp Pro Ala
 565 570 575
 Ile Leu Ser Lys Leu Ala Asp Leu Tyr Asp Gln Glu Gly Asp Lys Ser
 580 585 590
 Gln Ala Phe Gln Cys His Tyr Asp Ser Tyr Arg Tyr Phe Pro Ser Asn
 595 600 605
 Leu Glu Thr Val Glu Trp Leu Ala Ser Tyr Tyr Leu Glu Thr Gln Phe
 610 615 620
 Ser Glu Lys Ser Ile Asn Tyr Leu Glu Lys Ala Ala Leu Met Gln Pro
 625 630 635 640
 Asn Val Ser Lys Trp Gln Met Met Ile Ala Ser Cys Leu Arg Arg Thr
 645 650 655
 Gly Asn Tyr Gln Arg Ala Phe Glu Leu Tyr Arg Gln Ile His Arg Lys
 660 665 670
 Phe Pro Gln Asp Leu Asp Cys Leu Lys Phe Leu Val Arg Ile Ala Gly
 675 680 685
 Asp Leu Gly Met Thr Glu Tyr Lys Glu Tyr Lys Asp Lys Leu Glu Lys
 690 695 700
 Ala Glu Lys Ile Asn Gln Leu Arg Leu Gln Arg Glu Ser Asp Ser Ser
 705 710 715 720
 Gln Gly Lys Arg His Ser Ala Asn Ser Thr His Ser Leu Pro Pro Ser
 725 730 735
 Gly Leu Thr Gly Leu Gly Ser Gly Ser Gly Ser Ser Gly Gly Gly
 740 745 750
 Thr Arg Gln Tyr Ser Ala His Val Pro Leu Leu Leu Asp Ser Gly Thr
 755 760 765
 Pro Phe Thr Val Ala Gln Arg Asp Met Lys Ala Glu Asp Phe Ser Tyr
 770 775 780
 Asp Asp Pro Val Ala Ile Ser Ser Arg Pro Lys Thr Gly Thr Arg Lys
 785 790 795 800
 Thr Thr Thr Asp Thr Asn Ile Asp Asp Phe Gly Asp Phe Asp Asp Ser
 805 810 815
 Leu Leu Pro Asp
 820

<210> 36
 <211> 1198
 <212> PRT
 <213> Homo sapiens

<400> 36

Thr Leu Leu Gln Pro Leu Lys Gly His Lys Asp Thr Val Tyr Cys Val
 1 5 10 15
 Ala Tyr Ala Lys Asp Gly Lys Arg Phe Ala Ser Gly Ser Ala Asp Lys
 20 25 30
 Ser Val Ile Ile Trp Thr Ser Lys Leu Glu Gly Ile Leu Lys Tyr Thr
 35 40 45
 His Asn Asp Ala Ile Gln Cys Val Ser Tyr Asn Pro Ile Thr His Gln
 50 55 60
 Leu Ala Ser Cys Ser Ser Asp Phe Gly Leu Trp Ser Pro Glu Gln
 65 70 75 80
 Lys Ser Val Ser Lys His Lys Ser Ser Ser Lys Ile Ile Cys Cys Ser
 85 90 95
 Trp Thr Asn Asp Gly Gln Tyr Leu Ala Leu Gly Met Phe Asn Gly Ile
 100 105 110
 Ile Ser Ile Arg Asn Lys Asn Gly Glu Glu Lys Val Lys Ile Glu Arg
 115 120 125
 Pro Gly Gly Ser Leu Ser Pro Ile Trp Ser Ile Cys Trp Asn Pro Ser
 130 135 140
 Ser Arg Trp Glu Ser Phe Trp Met Asn Arg Glu Asn Glu Asp Ala Glu
 145 150 155 160
 Asp Val Ile Val Asn Arg Tyr Ile Gln Glu Ile Pro Ser Thr Leu Lys
 165 170 175
 Ser Ala Val Tyr Ser Ser Gln Gly Ser Glu Ala Glu Glu Glu Pro
 180 185 190
 Glu Glu Glu Asp Asp Ser Pro Arg Asp Asp Asn Leu Glu Glu Arg Asn
 195 200 205
 Asp Ile Leu Ala Val Ala Asp Trp Gly Gln Lys Val Ser Phe Tyr Gln
 210 215 220
 Leu Ser Gly Lys Gln Ile Gly Lys Asp Arg Ala Leu Asn Phe Asp Pro
 225 230 235 240
 Cys Cys Ile Ser Tyr Phe Thr Lys Gly Glu Tyr Ile Leu Leu Gly Gly
 245 250 255
 Ser Asp Lys Gln Val Ser Leu Phe Thr Lys Asp Gly Val Arg Leu Gly
 260 265 270
 Thr Val Gly Glu Gln Asn Ser Trp Val Trp Thr Cys Gln Ala Lys Pro
 275 280 285
 Asp Ser Asn Tyr Val Val Val Gly Cys Gln Asp Gly Thr Ile Ser Phe
 290 295 300
 Tyr Gln Leu Ile Phe Ser Thr Val His Gly Leu Tyr Lys Asp Arg Tyr
 305 310 315 320
 Ala Tyr Arg Asp Ser Met Thr Asp Val Ile Val Gln His Leu Ile Thr
 325 330 335
 Glu Gln Lys Val Arg Ile Lys Cys Lys Glu Leu Val Lys Lys Ile Ala
 340 345 350
 Ile Tyr Arg Asn Arg Leu Ala Ile Gln Leu Pro Glu Lys Ile Leu Ile
 355 360 365
 Tyr Glu Leu Tyr Ser Glu Asp Leu Ser Asp Met His Tyr Arg Val Lys
 370 375 380
 Glu Lys Ile Ile Lys Lys Phe Glu Cys Asn Leu Leu Val Val Cys Ala
 385 390 395 400
 Asn His Ile Ile Leu Cys Gln Glu Lys Arg Leu Gln Cys Leu Ser Phe
 405 410 415
 Ser Gly Val Lys Glu Arg Glu Trp Gln Met Glu Ser Leu Ile Arg Tyr
 420 425 430
 Ile Lys Val Ile Gly Gly Pro Pro Gly Arg Glu Gly Leu Leu Val Gly
 435 440 445

Leu Lys Asn Gly Gln Ile Leu Lys Ile Phe Val Asp Asn Leu Phe Ala
 450 455 460
 Ile Val Leu Leu Lys Gln Ala Thr Ala Val Arg Cys Leu Asp Met Ser
 465 470 475 480
 Ala Ser Arg Lys Lys Leu Ala Val Val Asp Glu Asn Asp Thr Cys Leu
 485 490 495
 Val Tyr Asp Ile Asp Thr Lys Glu Leu Leu Phe Gln Glu Pro Asn Ala
 500 505 510
 Asn Ser Val Ala Trp Asn Thr Gln Cys Glu Asp Met Leu Cys Phe Ser
 515 520 525
 Gly Gly Gly Tyr Leu Asn Ile Lys Ala Ser Thr Phe Pro Val His Arg
 530 535 540
 Gln Lys Leu Gln Gly Phe Val Val Gly Tyr Asn Gly Ser Lys Ile Phe
 545 550 555 560
 Cys Leu His Val Phe Ser Ile Ser Ala Val Glu Val Pro Gln Ser Ala
 565 570 575
 Pro Met Tyr Gln Tyr Leu Asp Arg Lys Leu Phe Lys Glu Ala Tyr Gln
 580 585 590
 Ile Ala Cys Leu Gly Val Thr Asp Thr Asp Trp Arg Glu Leu Ala Met
 595 600 605
 Glu Ala Leu Glu Gly Leu Asp Phe Glu Thr Ala Lys Lys Ala Phe Ile
 610 615 620
 Arg Val Gln Asp Leu Arg Tyr Leu Glu Leu Ile Ser Ser Ile Glu Glu
 625 630 635 640
 Arg Lys Lys Arg Gly Glu Thr Asn Asn Asp Leu Phe Leu Ala Asp Val
 645 650 655
 Phe Ser Tyr Gln Gly Lys Phe His Glu Ala Ala Lys Leu Tyr Lys Arg
 660 665 670
 Ser Gly His Glu Asn Leu Ala Leu Glu Met Tyr Thr Asp Leu Cys Met
 675 680 685
 Phe Glu Tyr Ala Lys Asp Phe Leu Gly Ser Gly Asp Pro Lys Glu Thr
 690 695 700
 Lys Met Leu Ile Thr Lys Gln Ala Asp Trp Ala Arg Asn Ile Lys Glu
 705 710 715 720
 Pro Lys Ala Ala Val Glu Met Tyr Ile Ser Ala Gly Glu His Val Lys
 725 730 735
 Ala Ile Glu Ile Cys Gly Asp His Gly Trp Val Asp Met Leu Ile Asp
 740 745 750
 Ile Ala Arg Lys Leu Asp Lys Ala Glu Arg Glu Pro Leu Leu Leu Cys
 755 760 765
 Ala Thr Tyr Leu Lys Lys Leu Asp Ser Pro Gly Tyr Ala Ala Glu Thr
 770 775 780
 Tyr Leu Lys Met Gly Asp Leu Lys Ser Leu Val Gln Leu His Val Glu
 785 790 795 800
 Thr Gln Arg Trp Asp Glu Ala Phe Ala Leu Gly Glu Lys His Pro Glu
 805 810 815
 Phe Lys Asp Asp Ile Tyr Met Pro Tyr Ala Gln Trp Leu Ala Glu Asn
 820 825 830
 Asp Arg Phe Glu Glu Ala Gln Lys Ala Phe His Lys Ala Gly Arg Gln
 835 840 845
 Arg Glu Ala Val Gln Val Leu Glu Gln Leu Thr Asn Asn Ala Val Ala
 850 855 860
 Glu Ser Arg Phe Asn Asp Ala Ala Tyr Tyr Tyr Trp Met Leu Ser Met
 865 870 875 880
 Gln Cys Leu Asp Ile Ala Gln Asp Pro Ala Gln Lys Asp Thr Met Leu
 885 890 895

Gly Lys Phe Tyr His Phe Gln Arg Leu Ala Glu Leu Tyr His Gly Tyr
 900 905 910
 His Ala Ile His Arg His Thr Glu Asp Pro Phe Ser Val His Arg Pro
 915 920 925
 Glu Thr Leu Phe Asn Ile Ser Arg Phe Leu Leu His Ser Leu Pro Lys
 930 935 940
 Asp Thr Pro Ser Gly Ile Ser Lys Val Lys Ile Leu Phe Thr Leu Ala
 945 950 955 960
 Lys Gln Ser Lys Ala Leu Gly Ala Tyr Arg Leu Ala Arg His Ala Tyr
 965 970 975
 Asp Lys Leu Arg Gly Leu Tyr Ile Pro Ala Arg Phe Gln Lys Ser Ile
 980 985 990
 Glu Leu Gly Thr Leu Thr Ile Arg Ala Lys Pro Phe His Asp Ser Glu
 995 1000 1005
 Glu Leu Val Pro Leu Cys Tyr Arg Cys Ser Thr Asn Asn Pro Leu Leu
 1010 1015 1020
 Asn Asn Leu Gly Asn Val Cys Ile Asn Cys Arg Gln Pro Phe Ile Phe
 1025 1030 1035 1040
 Ser Ala Ser Ser Tyr Asp Val Leu His Leu Val Glu Phe Tyr Leu Glu
 1045 1050 1055
 Glu Gly Ile Thr Asp Glu Glu Ala Ile Ser Leu Ile Asp Leu Glu Val
 1060 1065 1070
 Leu Arg Pro Lys Arg Asp Asp Arg Gln Leu Glu Ile Ala Asn Asn Ser
 1075 1080 1085
 Ser Gln Ile Leu Arg Leu Val Glu Thr Lys Asp Ser Ile Gly Asp Glu
 1090 1095 1100
 Asp Pro Phe Thr Ala Lys Leu Ser Phe Glu Gln Gly Gly Ser Glu Phe
 1105 1110 1115 1120
 Val Pro Val Val Val Ser Arg Leu Val Leu Arg Ser Met Ser Arg Arg
 1125 1130 1135
 Asp Val Leu Ile Lys Arg Trp Pro Pro Pro Leu Arg Trp Gln Tyr Phe
 1140 1145 1150
 Arg Ser Leu Leu Pro Asp Ala Ser Ile Thr Met Cys Pro Ser Cys Phe
 1155 1160 1165
 Gln Met Phe His Ser Glu Asp Tyr Glu Leu Leu Val Leu Gln His Gly
 1170 1175 1180
 Cys Cys Pro Tyr Cys Arg Arg Cys Lys Asp Asp Pro Gly Pro
 1185 1190 1195

<210> 37
<211> 1047
<212> PRT
<213> Caenorhabditis elegans

<400> 37
 Met Thr Met Lys Lys Ile Ser Arg Lys Leu Gly Phe His Gly Glu Gln
 1 5 10 15
 Val Cys Ile Tyr Asp Leu Ala Phe Lys Pro Asp Gly Ser Glu Leu Leu
 20 25 30
 Leu Ala Ala Asp Asn Lys Val Tyr Leu Phe Asp Val Asn Glu Gly Gly
 35 40 45
 Gln Met Gln Thr Leu Lys Gly His Lys Asp Leu Val Tyr Thr Val Ala
 50 55 60
 Trp Ser His Asn Gly Glu Leu Phe Ala Ser Gly Gly Ala Asp Lys Leu
 65 70 75 80
 Val Ile Leu Trp Asn Glu Lys His Glu Gly Thr Leu Arg Tyr Ser His
 85 90 95

Thr Asp Val Ile Gln Cys Met Met Phe Asn Pro Cys Asn Gln Ile Leu
 100 105 110
 Leu Thr Cys Ala Leu Asn Glu Phe Gly Leu Trp Ser Thr Ala Asp Lys
 115 120 125
 Asn Val Ile Lys Gln Arg Ser Val Val Arg Cys Cys Ser Cys Ala Trp
 130 135 140
 Asn Thr Asp Gly Thr Ile Phe Ala Ile Gly His Gly Asp Gly Thr Ile
 145 150 155 160
 Thr Leu Arg Lys Gly Thr Asn Ala Thr Glu Glu Pro Ser Ile Ile Ile
 165 170 175
 Gln Arg Asp Asn Glu Pro Ile Trp Gly Ile Ala Phe Ser Ser Asn Arg
 180 185 190
 Thr Phe Ala Ser Arg Asp Ser Gln Gly Asn Pro Met Gly Ile Asp Glu
 195 200 205
 Ile Met Ala Val Ile Asp Trp Asn Lys Thr Leu Ser Phe Tyr Ser Leu
 210 215 220
 Asp Gly Thr Phe Ile Glu Ser Lys Asn Leu Glu Phe Glu Pro His Cys
 225 230 235 240
 Ile Ser Tyr Cys Leu Asn Gly Glu Tyr Leu Leu Ile Gly Gly Ser Asp
 245 250 255
 Lys Ile Leu Lys Ile Tyr Thr Arg Lys Gly Val Leu Leu Gly Thr Val
 260 265 270
 Ala Gln Met Asp His Trp Ile Trp Ser Val Thr Val Arg Pro Asn Ser
 275 280 285
 Gln Thr Val Ala Met Gly Cys Val Asp Gly Thr Ile Ala Cys Tyr Asn
 290 295 300
 Leu Val Phe Ser Thr Val His Cys Val Asp His Ala Arg Tyr Ala Asn
 305 310 315 320
 Arg Lys Ser Met Thr Asp Val Phe Val Gln Asn Leu Glu Tyr Arg Thr
 325 330 335
 Ser Ser Asn Ile Cys Cys His Asp Leu Val Lys Lys Met Ser Leu Tyr
 340 345 350
 Asp Thr Lys Leu Ala Val Gln Leu Ser Asp Lys Ile Gln Ile Tyr Lys
 355 360 365
 Gln Thr Gly Gly Val Ser Lys Asn Glu Arg Arg Lys Gln Leu Lys Tyr
 370 375 380
 Thr Leu Gln Asp Thr Ile Arg Lys Asp Leu Ser Phe Ser Leu Met Val
 385 390 395 400
 Val Thr His Gly His Leu Val Val Cys Asn Asp Glu Lys Leu Glu Cys
 405 410 415
 Tyr Asp Phe Lys Gly Ile Lys Lys Arg Ser Trp Asn Met Lys Ser Ile
 420 425 430
 Val Arg Tyr Leu Arg Val Leu Gly Gly Pro Ala His Arg Glu Thr Leu
 435 440 445
 Val Leu Gly Thr Thr Asp Gly Gly Val Tyr Lys Val Phe Ile Asp Asn
 450 455 460
 Asp Tyr Pro Ile Leu Leu Asp Ser Arg Lys Thr Ala Ile Lys Cys Ile
 465 470 475 480
 Asp Ile Asn Ala Asn Arg Thr Val Leu Ala Ser Ile Glu Asp Thr Leu
 485 490 495
 Val Cys Lys Trp Ser Asp Ile Ala Thr Gly Glu Thr Leu Leu Gln Glu
 500 505 510
 Pro Gly Cys Tyr Ser Val Val Phe Asn Thr Val Asn Glu Asn Leu Phe
 515 520 525
 Ala Phe Thr Thr Asn Asn Met Leu His Val Arg Thr Leu Ala Ala Pro
 530 535 540

Asn Lys Val Phe Asp Leu Asp Asp Phe Glu Met Ala Cys Leu Arg Lys
 995 1000 1005
 Gly His Cys Pro Phe Cys Arg Thr Ser Tyr Asp Arg Asn Glu Ala Phe
 1010 1015 1020
 Phe Val Asp Glu Glu Asp Glu Asp Asn Thr Asn Ile Pro Ser Phe
 1025 1030 1035 1040
 Gly Gln Phe Ser Arg Phe Ser
 1045

<210> 38
 <211> 1386
 <212> PRT
 <213> Homo sapiens

<400> 38
 Ser Phe Ile Gln Ala Gly Ile Ile Tyr Tyr Ser Gln Glu Lys Tyr Phe
 1 5 10 15
 His His Val Gln Ala Ala Ala Val Gly Leu Glu Lys Phe Ser Asn Asp
 20 25 30
 Pro Val Leu Lys Phe Phe Lys Ala Tyr Gly Val Leu Lys Glu Asp Arg
 35 40 45
 Glu Ala Ile Gln Glu Leu Glu Tyr Ser Leu Lys Glu Ile Arg Lys Thr
 50 55 60
 Val Ser Gly Thr Ala Leu Tyr Tyr Ala Gly Leu Phe Leu Trp Leu Ile
 65 70 75 80
 Gly Arg His Asp Lys Ala Lys Glu Tyr Ile Asp Arg Met Leu Lys Ile
 85 90 95
 Ser Arg Gly Phe Arg Glu Ala Tyr Val Leu Arg Gly Trp Val Asp Leu
 100 105 110
 Thr Ser Asp Lys Pro His Thr Ala Lys Lys Ala Ile Glu Tyr Leu Glu
 115 120 125
 Gln Gly Ile Gln Asp Thr Lys Asp Val Leu Gly Leu Met Gly Lys Ala
 130 135 140
 Met Tyr Phe Met Met Gln Gln Asn Tyr Ser Glu Ala Leu Glu Val Val
 145 150 155 160
 Asn Gln Ile Thr Val Thr Ser Gly Ser Phe Leu Pro Ala Leu Val Leu
 165 170 175
 Lys Met Gln Leu Phe Leu Ala Arg Gln Asp Trp Glu Gln Thr Val Glu
 180 185 190
 Met Gly His Arg Arg Ile Leu Glu Lys Asp Glu Ser Asn Ile Asp Ala
 195 200 205
 Cys Gln Ile Leu Thr Val His Glu Leu Ala Arg Glu Gly Asn Met Thr
 210 215 220
 Thr Gln Ala Thr Asn His Val Arg Asn Leu Ile Lys Ala Leu Glu Thr
 225 230 235 240
 Arg Glu Pro Glu Asn Pro Ser Leu His Leu Lys Lys Ile Ile Val Val
 245 250 255
 Ser Arg Leu Val Cys Gly Ser His Gln Val Ile Leu Gly Leu Val Cys
 260 265 270
 Ser Phe Ile Glu Arg Thr Phe Met Ala Thr Pro Ser Tyr Val His Val
 275 280 285
 Ala Thr Glu Leu Gly Tyr Leu Phe Ile Leu Lys Asn Gln Val Lys Glu
 290 295 300
 Ala Leu Leu Trp Tyr Ser Glu Ala Met Lys Leu Asp Lys Asp Gly Met
 305 310 315 320
 Ala Gly Leu Thr Gly Ile Ile Leu Cys His Ile Leu Glu Gly His Leu
 325 330 335

Glu Glu Ala Glu Tyr Arg Leu Glu Phe Leu Lys Glu Val Gln Lys Ser
 340 345 350
 Leu Gly Lys Ser Glu Val Arg Ala Pro Trp Gly Tyr Gly Leu Leu Gln
 355 360 365
 Asp Asp Val Leu Cys Cys Pro Pro Thr Pro Thr Phe Gln Cys Lys Val
 370 375 380
 Ala Trp Thr Phe Thr Leu Pro Leu Pro Thr Lys Ser Ala Gln Ala Asp
 385 390 395 400
 Ile Gly Thr Glu Thr Arg Ser Ser Leu Pro Gln Val Leu Ile Phe Leu
 405 410 415
 Gln Ala Leu Leu Met Ser Arg Lys His Lys Gly Glu Glu Thr Thr
 420 425 430
 Ala Leu Leu Lys Glu Ala Val Glu Leu His Phe Ser Ser Met Gln Gly
 435 440 445
 Ile Pro Leu Gly Ser Glu Tyr Phe Glu Lys Leu Asp Pro Tyr Phe Leu
 450 455 460
 Val Cys Ile Ala Lys Glu Tyr Leu Leu Phe Cys Pro Lys Gln Pro Arg
 465 470 475 480
 Leu Pro Gly Gln Ile Val Ser Pro Leu Leu Lys Gln Val Ala Val Ile
 485 490 495
 Leu Asn Pro Val Val Lys Ala Ala Pro Ala Leu Ile Asp Pro Leu Tyr
 500 505 510
 Leu Met Ala Gln Val Arg Tyr Tyr Ser Gly Glu Leu Glu Asn Ala Gln
 515 520 525
 Ser Ile Leu Gln Arg Cys Leu Glu Leu Asp Pro Ala Ser Val Asp Ala
 530 535 540
 His Leu Leu Met Cys Gln Ile Tyr Leu Ala Gln Gly Asn Phe Gly Met
 545 550 555 560
 Cys Phe His Cys Leu Glu Leu Gly Val Ser His Asn Phe Gln Val Val
 565 570 575
 Arg Asp His Pro Leu Tyr His Leu Ile Lys Ala Arg Ala Leu Asn Lys
 580 585 590
 Ala Gly Asp Tyr Pro Glu Ala Ile Lys Thr Leu Lys Met Val Ile Lys
 595 600 605
 Leu Pro Ala Leu Lys Lys Glu Glu Gly Arg Lys Phe Leu Arg Pro Ser
 610 615 620
 Val Gln Pro Ser Gln Arg Ala Ser Ile Leu Leu Glu Leu Val Glu Ala
 625 630 635 640
 Leu Arg Leu Asn Gly Glu Leu His Glu Ala Thr Lys Val Met Gln Asp
 645 650 655
 Thr Ile Asn Glu Phe Gly Gly Thr Pro Glu Glu Asn Arg Ile Thr Ile
 660 665 670
 Ala Asn Val Asp Leu Val Leu Ser Lys Gly Asn Val Asp Val Ala Leu
 675 680 685
 Asn Met Leu Arg Asn Ile Leu Pro Lys Gln Ser Cys Tyr Met Glu Ala
 690 695 700
 Arg Glu Lys Met Ala Asn Ile Tyr Leu Gln Thr Leu Arg Asp Arg Arg
 705 710 715 720
 Leu Tyr Ile Arg Cys Tyr Glu Leu Cys Glu His Leu Pro Gly Pro His
 725 730 735
 Thr Ser Leu Leu Leu Gly Asp Ala Leu Met Ser Ile Leu Glu Val Ser
 740 745 750
 Glu Arg Pro His Ser Leu Ala Lys Trp Pro Pro Ser Leu Pro Ser Pro
 755 760 765
 Val Gly Glu Lys Arg Lys Thr Gln Arg His Phe Pro His Gln Pro Glu
 770 775 780

Lys Ala Leu Glu Val Tyr Asp Glu Ala Tyr Arg Gln Asn Pro His Asp
 785 790 795 800
 Ala Ser Leu Ala Ser Arg Ile Gly His Ala Tyr Val Lys Ala His Gln
 805 810 815
 Tyr Thr Lys Ala Ile Glu Tyr Tyr Glu Ala Ala Gln Lys Ile Asn Gly
 820 825 830
 Gln Asp Phe Leu Cys Cys Asp Leu Gly Lys Leu Leu Lys Leu Lys
 835 840 845
 Lys Val Asn Lys Ala Glu Lys Val Leu Lys Gln Ala Leu Glu His Asp
 850 855 860
 Ile Gly Val Gln Asp Ile Pro Ser Met Met Asn Asp Val Lys Cys Leu
 865 870 875 880
 Leu Leu Leu Ala Lys Val Tyr Lys Ser His Lys Lys Glu Ala Val Ile
 885 890 895
 Glu Thr Leu Asn Lys Val Ile Asp Arg Trp Thr Gln Ala Leu Ala Leu
 900 905 910
 Asp Leu Gln Ser Arg Ile Leu Lys Arg Val Pro Leu Glu Gln Pro Glu
 915 920 925
 Met Ile Pro Ser Gln Lys Gln Leu Ala Ala Ser Ile Cys Ile Gln Phe
 930 935 940
 Ala Glu His Tyr Leu Ala Glu Lys Glu Tyr Asp Lys Ala Val Gln Ser
 945 950 955 960
 Tyr Lys Asp Val Phe Ser Tyr Leu Pro Thr Asp Asn Lys Val Leu Met
 965 970 975
 Ala Asp Leu Met Phe Arg Lys Gln Lys His Glu Ala Ala Ile Asn Leu
 980 985 990
 Tyr His Gln Val Leu Glu Lys Ala Pro Gly Asp Asn Phe Leu Val Leu
 995 1000 1005
 His Lys Leu Ile Asp Leu Leu Arg Arg Ser Gly Lys Leu Glu Asp Ile
 1010 1015 1020
 Pro Ala Phe Phe Glu Leu Ala Lys Lys Val Ser Ser Arg Val Pro Leu
 1025 1030 1035 1040
 Glu Pro Gly Phe Asn Tyr Cys Arg Gly Ile Tyr Cys Trp His Ile Gly
 1045 1050 1055
 Gln Pro Asn Glu Ala Leu Lys Phe Leu Asn Lys Ala Arg Lys Asp Ser
 1060 1065 1070
 Thr Trp Gly Gln Ser Ala Ile Tyr His Met Val Gln Ile Cys Leu Asn
 1075 1080 1085
 Pro Asp Asn Glu Val Val Gly Gly Glu Ala Phe Glu Asn Leu Ile Pro
 1090 1095 1100
 Arg Ser Asn Thr Cys Ser Tyr Met Glu Lys Lys Glu Leu Glu Gln Gln
 1105 1110 1115 1120
 Gly Val Ser Thr Ala Glu Lys Leu Leu Arg Glu Phe Tyr Pro His Ser
 1125 1130 1135
 Asp Ser Ser Gln Thr Gln Leu Arg Leu Leu Gln Gly Leu Cys Arg Leu
 1140 1145 1150
 Ala Thr Arg Glu Lys Ala Asn Met Glu Ala Ala Leu Gly Ser Phe Ile
 1155 1160 1165
 Gln Ile Ala Gln Ala Glu Lys Asp Ser Val Pro Ala Leu Leu Ala Leu
 1170 1175 1180
 Ala Gln Ala Tyr Val Phe Leu Lys Gln Ile Pro Lys Ala Arg Met Gln
 1185 1190 1195 1200
 Leu Lys Arg Leu Ala Lys Thr Pro Trp Val Leu Ser Glu Ala Glu Asp
 1205 1210 1215
 Leu Glu Lys Ser Trp Leu Leu Leu Ala Asp Ile Tyr Cys Gln Gly Ser
 1220 1225 1230

Lys Phe Asp Leu Ala Leu Glu Leu Leu Arg Arg Cys Val Gln Tyr Asn
 1235 1240 1245
 Lys Ala Gln Ser Cys Tyr Lys Ala Tyr Glu Tyr Met Gly Phe Ile Met
 1250 1255 1260
 Glu Lys Glu Gln Ser Tyr Lys Asp Ala Val Thr Asn Tyr Lys Leu Ala
 1265 1270 1275 1280
 Trp Lys Tyr Ser His His Ala Asn Pro Ala Ile Gly Lys Ala Thr Ser
 1285 1290 1295
 Gln Gly Ala Arg Glu Thr Trp Glu Gly Gly Gln Glu Pro His His
 1300 1305 1310
 Asp Pro Arg Thr Gln Gly Leu Tyr Pro Gly Cys Tyr Glu Asn Gln Arg
 1315 1320 1325
 Gly Ser Gln Val Thr Arg Val Pro Pro Ser Leu Leu Ser Met Ser Pro
 1330 1335 1340
 Val Gly Phe Lys Leu Ala Phe Asn Tyr Leu Lys Asp Lys Lys Phe Val
 1345 1350 1355 1360
 Glu Ala Ile Glu Ile Cys Asn Asp Val Ser Gln Gln Pro Trp Trp Gly
 1365 1370 1375
 Gly Pro Gly Val Val Val Gly Asn Pro Ala
 1380 1385


 <210> 39
 <211> 1008
 <212> PRT
 <213> Homo sapiens

<400> 39
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 Tyr His Ala Tyr Gly Thr Leu Met Glu Gly Lys Thr Gln Glu Ala Leu
 35 40 45
 Arg Glu Phe Glu Ala Ile Lys Asn Lys Gln Asp Val Ser Leu Cys Ser
 50 55 60
 Leu Leu Ala Leu Ile Tyr Ala His Lys Asp Arg Glu Ala Ile Leu Glu
 65 70 75 80
 Ser Asp Ala Arg Val Lys Glu Gln Arg Lys Gly Ala Gly Glu Lys Ala
 85 90 95
 Leu Tyr His Ala Gly Leu Phe Leu Trp His Ile Gly Arg His Asp Lys
 100 105 110
 Ala Arg Glu Tyr Ile Asp Arg Met Ile Lys Ile Ser Asp Gly Ser Lys
 115 120 125
 Gln Gly His Val Leu Lys Ala Trp Leu Asp Ile Thr Arg Gly Lys Glu
 130 135 140
 Pro Tyr Thr Lys Lys Ala Leu Lys Tyr Phe Glu Glu Gly Leu Gln Asp
 145 150 155 160
 Gly Asn Asp Thr Phe Ala Leu Leu Gly Lys Val Ser Trp Arg Gln Asn
 165 170 175
 Tyr Ser Gly Ala Leu Glu Thr Val Asn Gln Ile Ile Val Asn Phe Pro
 180 185 190
 Ser Phe Leu Pro Ala Phe Val Lys Lys Met Lys Leu Gln Leu Ala Leu
 195 200 205
 Gln Asp Trp Asp Gln Thr Val Glu Thr Ala Gln Arg Leu Ser Asn Lys
 210 215 220
 Ile Ile Phe Phe Ser Phe Cys Gly Arg Ser Gln Leu Ile Leu Gln Lys
 225 230 235 240

Ile Gln Thr Leu Leu Glu Arg Ala Phe Ser Leu Asn Pro Gln Gln Ser
 245 250 255
 Glu Phe Ala Thr Glu Leu Gly Tyr Gln Met Ile Leu Gln Gly Arg Val
 260 265 270
 Lys Glu Ala Leu Lys Trp Tyr Lys Thr Ala Met Thr Leu Asp Glu Thr
 275 280 285
 Ser Val Ser Ala Leu Val Gly Phe Ile Gln Cys Gln Leu Ile Glu Gly
 290 295 300
 Gln Leu Gln Asp Ala Asp Gln Gln Leu Glu Phe Leu Asn Glu Ile Gln
 305 310 315 320
 Gln Ser Ile Gly Lys Ser Ala Val Leu Ile Tyr Leu His Ala Val Leu
 325 330 335
 Ala Met Lys Lys Asn Lys Arg Gln Glu Glu Val Ile Asn Leu Leu Asn
 340 345 350
 Asp Val Leu Asp Thr His Phe Ser Gln Leu Glu Gly Leu Pro Leu Gly
 355 360 365
 Ile Gln Tyr Phe Glu Lys Leu Asn Pro Asp Phe Leu Leu Glu Ile Val
 370 375 380
 Met Glu Tyr Leu Ser Phe Cys Pro Met Gln Val Ser Asn Tyr Gly Phe
 385 390 395 400
 Leu Leu Gly Asp Ile Glu Ala Ala Phe Asn Asn Leu Gln His Cys Leu
 405 410 415
 Glu His Asn Pro Ser Tyr Ala Asp Ala His Leu Leu Leu Ala Gln Val
 420 425 430
 Tyr Leu Ser Gln Glu Lys Val Lys Leu Cys Ser Gln Ser Leu Glu Leu
 435 440 445
 Cys Leu Ser Tyr Asp Phe Lys Val Gln Val Arg Asp Tyr Pro Leu Tyr
 450 455 460
 His Leu Ile Lys Ala Gln Ser Gln Lys Lys Met Gly Glu Ile Ala Asp
 465 470 475 480
 Ala Ile Lys Thr Leu His Met Ala Met Ser Leu Pro Gly Met Lys Arg
 485 490 495
 Ile Gly Ala Ser Thr Lys Ser Lys Asp Arg Lys Thr Glu Val Asp Thr
 500 505 510
 Ser His Arg Leu Ser Ile Phe Leu Glu Leu Ile Asp Val His Arg Leu
 515 520 525
 Asn Gly Glu His Glu Ala Thr Lys Val Leu Gln Asp Ala Ile His Glu
 530 535 540
 Phe Ser Gly Thr Ser Glu Glu Val Arg Val Thr Ile Ala Asn Ala Asp
 545 550 555 560
 Leu Ala Leu Ala Gln Gly Asp Ile Glu Arg Ala Leu Ser Ile Leu Gln
 565 570 575
 Asn Val Thr Ala Glu Gln Pro Tyr Phe Ile Glu Ala Arg Glu Lys Met
 580 585 590
 Ala Asp Ile Tyr Leu Lys His Arg Lys Asp Lys Met Leu Tyr Ile Thr
 595 600 605
 Cys Phe Ala Ile Thr Tyr Tyr Glu Ala Ala Leu Lys Thr Gly Gln Lys
 610 615 620
 Asn Tyr Leu Cys Tyr Asp Leu Ala Glu Leu Leu Lys Leu Lys Trp
 625 630 635 640
 Tyr Asp Lys Ala Glu Lys Val Leu Gln His Ala Leu Ala His Glu Pro
 645 650 655
 Gly Met Lys Ala Arg Glu Leu Gln Ala Arg Val Leu Lys Arg Val Gln
 660 665 670
 Met Glu Gln Pro Asp Ala Val Pro Ala Gln Lys His Leu Ala Ala Glu
 675 680 685

Ile Cys Ala Glu Ile Ala Lys His Ser Val Ala Gln Arg Asp Tyr Glu
 690 695 700
 Lys Ala Ile Lys Phe Tyr Arg Glu Ala Leu Val His Cys Glu Thr Asp
 705 710 715 720
 Asn Lys Val Asp Asn Tyr Met Thr Leu Ser Arg Leu Ile Asp Leu Leu
 725 730 735
 Arg Arg Cys Gly Lys Leu Glu Asp Val Pro Arg Phe Phe Ser Met Ala
 740 745 750
 Glu Lys Arg Asn Ser Arg Ala Lys Leu Glu Pro Gly Phe Gln Tyr Cys
 755 760 765
 Lys Gly Leu Tyr Leu Trp Tyr Thr Gly Glu Pro Asn Asp Ala Leu Arg
 770 775 780
 His Phe Asn Lys Ala Arg Lys Asp Arg Asp Trp Gly Gln Asn Ala Leu
 785 790 795 800
 Tyr Asn Met Ile Glu Ile Cys Leu Asn Pro Asp Asn Glu Thr Val Gly
 805 810 815
 Gly Glu Val Phe Glu Asn Leu Asp Gly Asp Ser Asn Ser Thr Glu Lys
 820 825 830
 Gln Glu Ser Val Gln Leu Ala Val Arg Thr Ala Glu Lys Leu Leu Lys
 835 840 845
 Glu Leu Lys Pro Gln Thr Val Gln Gly His Val Gln Leu Arg Ile Met
 850 855 860
 Glu Asn Tyr Cys Leu Met Ala Thr Lys Gln Lys Ser Asn Val Glu Gln
 865 870 875 880
 Ala Leu Asn Thr Phe Thr Glu Ile Ala Ala Ser Glu Lys Glu His Ile
 885 890 895
 Pro Ala Leu Leu Gly Met Ala Thr Ala Tyr Met Ile Leu Lys Gln Thr
 900 905 910
 Pro Arg Ala Arg Asn Gln Leu Lys Arg Ile Ala Lys Met Asn Trp Asn
 915 920 925
 Ala Ile Asp Ala Glu Glu Phe Glu Lys Ser Trp Leu Leu Ala Asp
 930 935 940
 Ile Tyr Ile Gln Ser Ala Lys Tyr Asp Met Ala Glu Asp Leu Leu Lys
 945 950 955 960
 Arg Cys Leu Arg His Asn Arg Ser Cys Cys Lys Ala Tyr Glu Tyr Met
 965 970 975
 Gly Tyr Ile Met Glu Lys Glu Gln Ala Tyr Thr Asp Ala Ala Leu Asn
 980 985 990
 Tyr Glu Met Ala Trp Lys Tyr Ser Asn Arg Thr Asn Pro Ala Val Gly
 995 1000 1005

<210> 40

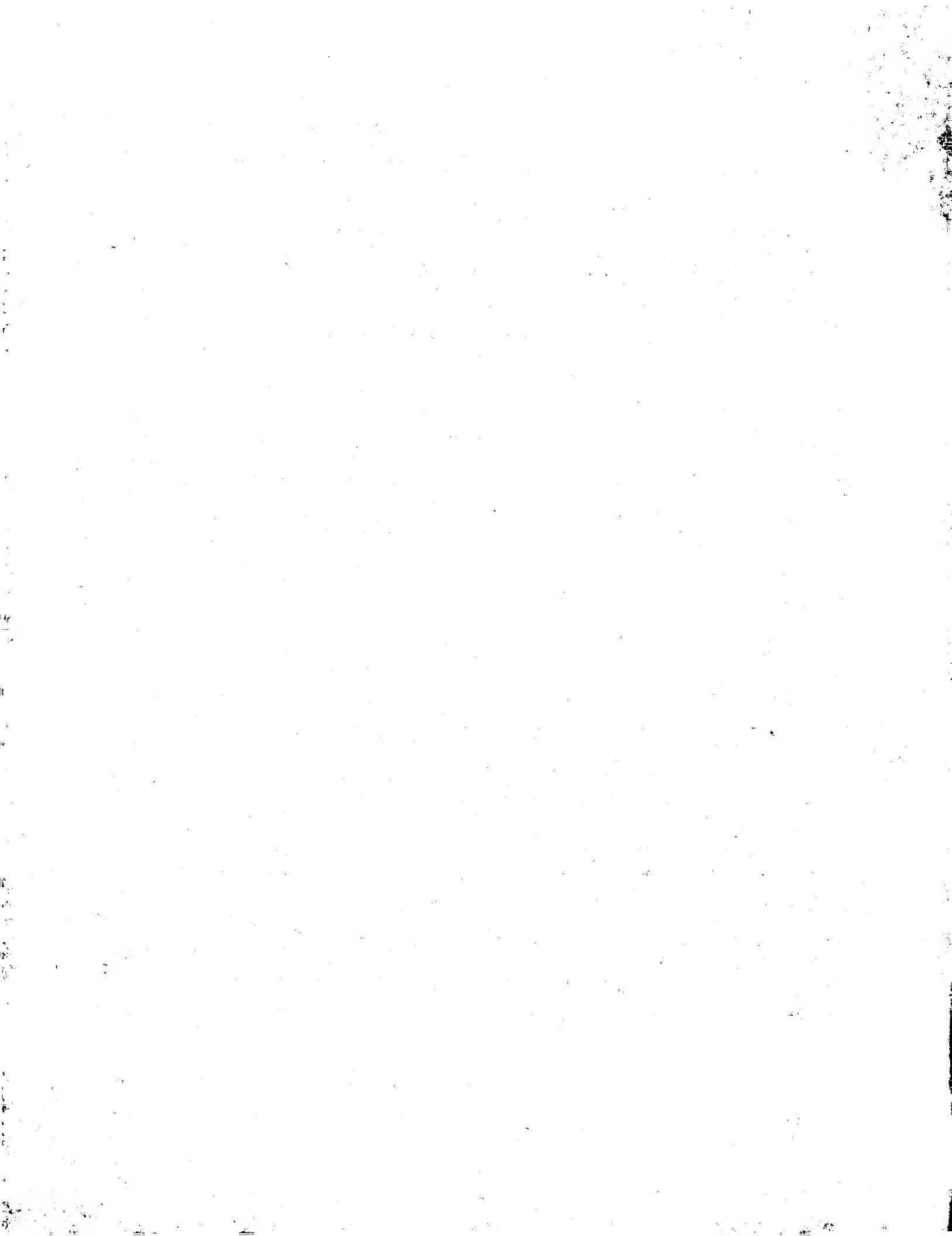
<211> 1115

<212> PRT

<213> Caenorhabditis elegans

<400> 40

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 Pro Gly His Ile Glu Lys Ala Lys Ala Ser Ile Met Met Lys Asp Trp
 20 25 30
 Arg Gly Val Met Asp Cys Ile Met Asn Ala Asp Gln Pro Glu Gly Ser
 35 40 45
 Asn Pro Tyr Ile Glu Val Leu Arg Thr Val His Gly Ile Cys Tyr Ala
 50 55 60
 Gly Glu Val Ser Met Leu Lys Arg Thr Leu Gln Leu Leu Lys Ser
 65 70 75 80



Leu Asp Glu Asn Glu Ala Thr Asn His Val Leu Tyr Ala Arg Ile Thr
 85 90 95
 Lys Leu Leu Val Ser Ile Ser Gly Arg Asp Glu Lys Ile Leu Arg His
 100 105 110
 Ala Arg Asp Phe Leu Thr Arg Ala Leu Lys Ile Ser Arg Lys Pro Asp
 115 120 125
 Tyr Val Ala Leu Ser Met Arg Ile Ala Phe Gly Leu Gly Ala Lys
 130 135 140
 Glu Val Ser Thr Leu Ser Gln Glu Leu Val Ala Leu Asp Cys Glu Asp
 145 150 155 160
 Ser Tyr Ala Val Leu Ser Ser Val Val Ser Met Leu Met Ile Ser Arg
 165 170 175
 Val Ser Asp Ala Arg Ala Gln Phe Asp Ile Leu Pro Ser Ala His Pro
 180 185 190
 Lys Leu Leu Glu Ser Pro Leu Tyr Tyr Leu Ile Ala Ser Val Leu Ala
 195 200 205
 Lys Gln Ser Lys Asp Lys Ser Phe Glu Asn Phe Arg Gln His Ile Glu
 210 215 220
 Asn Leu Val Glu Met Leu Arg Asn Gln Leu Gln Ser Phe Pro Phe Gly
 225 230 235 240
 Leu Asp Tyr Leu Ser Leu Phe Ser Ser Asp Leu Leu Tyr Ser Ala Val
 245 250 255
 Glu Gln Cys Phe Asp Phe Tyr Pro Leu Val Pro Ile Lys Ala Pro Asp
 260 265 270
 Asp Cys Met Lys Leu Thr Ala Lys Thr Leu Gln Met Ile Tyr Asp Val
 275 280 285
 Ala Pro Gly Leu Ala His Cys Thr Leu Gln Leu Ala Arg Asn Ser Tyr
 290 295 300
 Leu Cys Ser Asn Thr Asn Ala Ala Glu Lys Trp Ile Glu Lys Val Leu
 305 310 315 320
 Asp Lys Asp Asp Ser Leu Ala Asp Ala His Ile Leu Arg Ala Glu Leu
 325 330 335
 Ile Leu Asp Arg Gly Gly Lys Ile Thr Asp Ala Asp Asp Ala Leu Val
 340 345 350
 Thr Gly Leu Asn Phe Asn Phe Lys Leu Arg Glu Thr Ser Leu Tyr His
 355 360 365
 Leu Ile Lys Ser Lys Thr Phe Lys Lys Arg Asn Glu Asn Asp Glu Ala
 370 375 380
 Ile Lys Thr Leu Lys Met Ala Leu Gln Ile Pro Arg Lys Glu Pro Ser
 385 390 395 400
 Lys Asn Leu Phe Gln Pro Lys Glu Ser Ala Asp Thr His Lys Ile Ser
 405 410 415
 Val Gln Leu Glu Leu Ile Asp Thr Leu Gln His Met Lys Arg Ile Gln
 420 425 430
 Glu Ala Glu Thr Thr Met Thr Asp Ala Leu Ala Glu Trp Ala Gly Gln
 435 440 445
 Pro Glu Gln Asp Gln Leu Val Ile Ala Gln Ala Gln Leu Tyr Leu Thr
 450 455 460
 Lys Gly His Val Glu Arg Ala Leu Gly Ile Leu Lys Lys Ile Gln Pro
 465 470 475 480
 Gly Gln Ser Asn Phe His Leu Ser Arg Ile Lys Met Ala Glu Ile Tyr
 485 490 495
 Leu Glu Glu Lys Lys Asp Lys Arg Met Phe Ala Ala Cys Tyr Arg Glu
 500 505 510
 Leu Leu Lys Val Glu Ala Thr Pro Gly Ser Tyr Ser Leu Leu Gly Asp
 515 520 525

Ala Phe Met Lys Val Gln Glu Pro Glu Asp Ala Ile Asn Phe Tyr Glu
 530 535 540
 Gln Ala Leu Lys Met Gln Ser Lys Asp Val Gln Leu Ala Glu Lys Ile
 545 550 555 560
 Gly Glu Ala Tyr Val Met Ala His Leu Tyr Ser Lys Ala Val Asn Phe
 565 570 575
 Tyr Glu Ser Ser Met Asn Ile Tyr Lys Asp Lys Asn Met Arg Leu Lys
 580 585 590
 Leu Ala Asn Leu Leu Lys Leu Arg Asn Phe Glu Lys Cys Glu Lys
 595 600 605
 Val Leu Arg Ala Pro Phe Glu Arg Asp Pro Glu Pro Val Gly Thr Glu
 610 615 620
 Thr Ile Gln Thr Tyr Ile Gln Phe Leu Leu Leu Ala Glu Cys His
 625 630 635 640
 Glu Met Met Asp Asn Val Pro Glu Ala Met Asn Asp Phe Glu Lys Ala
 645 650 655
 Lys Ser Leu His Ser Arg Ile Gln Asp Lys Thr Leu Thr Ala Ala Leu
 660 665 670
 Lys Lys Glu Gly Ala Arg Ile Cys Asn Leu Gln Ala Glu Leu Leu Tyr
 675 680 685
 Arg Arg Arg Glu Phe Ser Gln Ala Val Asp Ile Cys Lys Gln Ala Leu
 690 695 700
 Ala Tyr His Glu Thr Asp Leu Lys Ala Asn Leu Leu Ser Lys Ile
 705 710 715 720
 Phe Lys Glu Glu Asn Lys Trp Thr Leu Val Leu Gln Pro Cys Gln Thr
 725 730 735
 Val Ile Gln Val Asp Pro His Asn Asp Glu Ala Asn Ser Ile Leu Ala
 740 745 750
 Asp Phe Tyr Tyr Ile Arg Ser Glu Ala Ala His Ala Ser Thr Ser Tyr
 755 760 765

 Thr Thr Leu Leu Asn Thr Asn Pro Gln His Trp His Ala Leu Ser Arg
 770 775 780
 Val Val Glu Leu Phe Cys Arg Asn Gly Glu Gln Asn Ala Ala Glu Lys
 785 790 795 800
 His Leu Asp Arg Ala Lys Glu Val Asn Pro Arg Cys Val Thr Glu Ser
 805 810 815
 Gly Tyr Asn Val Cys Arg Gly Arg Phe Glu Trp Tyr Thr Gly Asp Gln
 820 825 830
 Asn Glu Ala Leu Arg Tyr Tyr Ser Arg Thr Lys Asp Ser Ala Ala Gly
 835 840 845
 Trp Arg Glu Lys Ala Leu Tyr Tyr Met Ile Asp Ile Cys Leu Asn Pro
 850 855 860
 Asp Asn Glu Ile Ile Asp Glu Asn Ser Val Glu Asn Pro Glu Thr
 865 870 875 880
 Thr Lys Ile Ile Tyr Leu Val Ser Glu Leu Trp Lys Lys Leu Val Asn
 885 890 895
 Ser Lys Asn Leu Pro Asn Ile Thr Ser Ile Tyr Ser Glu Asn Phe Gln
 900 905 910
 Ser Thr Asp Arg Phe Leu Leu Ala Gln Asn Phe Ile Arg Met His Thr
 915 920 925
 Thr Asp Lys Ser Ala Ile Gln Ala Ala Leu Asp Glu Phe Asn Arg Met
 930 935 940
 Ala Phe Asn Ala Asp Arg Ser Gln Val Thr Asn Val Gly Ala Val Phe
 945 950 955 960
 Gly Val Ala Arg Gly His Val Leu Leu Lys Gln Val Gln Lys Ala Lys
 965 970 975

Thr Val Leu Lys Met Val Asn Gly Arg Val Trp Asn Phe Asp Asp Ser
 980 985 990
 Asp Tyr Leu Glu Lys Cys Trp Leu Met Leu Ala Asp Ile Tyr Ile Asn
 995 1000 1005
 Gln Asn Lys Asn Asp Gln Ala Val Thr Phe Leu Asp Leu Val Phe Lys
 1010 1015 1020
 Tyr Asn Cys Asn Cys Leu Lys Ala Phe Glu Leu Tyr Gly Tyr Met Arg
 1025 1030 1035 1040
 Glu Lys Glu Gln Lys Tyr Val Glu Ala Tyr Lys Met Tyr Glu Lys Ala
 1045 1050 1055
 Phe Met Ala Thr Lys Glu Arg Asn Pro Gly Phe Gly Tyr Lys Leu Ala
 1060 1065 1070
 Phe Thr Tyr Leu Lys Ala Lys Arg Leu Phe Ala Cys Ile Glu Thr Cys
 1075 1080 1085
 Gln Lys Val Leu Asp Leu Asn Pro Gln Tyr Pro Lys Ile Lys Lys Glu
 1090 1095 1100
 Ile Met Asp Lys Ala Lys Ala Leu Ile Arg Thr
 1105 1110 1115

<210> 41
 <211> 764
 <212> PRT
 <213> Homo sapiens

A4
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 Ser Cys Ser Asp Asp His Gln Ile Val Lys Trp Asn Leu Leu Thr Ser
 20 25 30
 Glu Thr Thr Gln Ile Val Lys Leu Pro Asp Asp Ile Tyr Pro Ile Asp
 35 40 45
 Phe His Trp Phe Pro Lys Ser Leu Gly Val Lys Lys Gln Thr Gln Ala
 50 55 60
 Glu Ser Phe Val Leu Thr Ser Ser Asp Gly Lys Phe His Leu Ile Ser
 65 70 75 80
 Lys Leu Gly Arg Val Glu Lys Ser Val Glu Ala His Cys Gly Ala Val
 85 90 95
 Leu Ala Gly Arg Trp Asn Tyr Glu Gly Thr Ala Leu Val Thr Val Gly
 100 105 110
 Glu Asp Gly Gln Ile Lys Ile Trp Ser Lys Thr Gly Met Leu Arg Ser
 115 120 125
 Thr Leu Ala Gln Gln Gly Thr Pro Val Tyr Ser Val Ala Trp Gly Pro
 130 135 140
 Asp Ser Glu Lys Val Leu Tyr Thr Ala Gly Lys Gln Leu Ile Ile Lys
 145 150 155 160
 Pro Leu Gln Pro Asn Ala Lys Val Leu Gln Trp Lys Ala His Asp Gly
 165 170 175
 Ile Ile Leu Lys Val Asp Trp Asn Ser Val Asn Asp Leu Ile Leu Ser
 180 185 190
 Ala Gly Glu Asp Cys Lys Tyr Lys Val Trp Asp Ser Tyr Gly Arg Pro
 195 200 205
 Leu Tyr Asn Ser Gln Pro His Glu His Pro Ile Thr Ser Val Ala Trp
 210 215 220
 Ala Pro Asp Gly Glu Leu Phe Ala Val Gly Ser Phe His Thr Leu Arg
 225 230 235 240
 Leu Cys Asp Lys Thr Gly Trp Ser Tyr Ala Leu Glu Lys Pro Asn Thr
 245 250 255

Gly Ser Ile Phe Asn Ile Ala Trp Ser Ile Asp Gly Thr Gln Ile Ala
 260 265 270
 Gly Ala Cys Gly Asn Gly His Val Val Phe Ala His Val Val Glu Gln
 275 280 285
 His Trp Glu Trp Lys Asn Phe Gln Val Thr Leu Thr Lys Arg Arg Ala
 290 295 300
 Met Gln Val Arg Asn Val Leu Asn Asp Ala Val Asp Leu Leu Glu Phe
 305 310 315 320
 Arg Asp Arg Val Ile Lys Ala Ser Leu Asn Tyr Ala His Leu Val Val
 325 330 335
 Ser Thr Ser Leu Gln Cys Tyr Val Phe Ser Thr Lys Asn Trp Asn Thr
 340 345 350
 Pro Ile Ile Phe Asp Leu Lys Glu Gly Thr Val Ser Leu Ile Leu Gln
 355 360 365
 Ala Glu Arg His Phe Leu Leu Val Asp Gly Ser Ser Ile Tyr Leu Tyr
 370 375 380
 Ser Tyr Glu Gly Arg Phe Ile Ser Ser Pro Lys Phe Pro Gly Met Arg
 385 390 395 400
 Thr Asp Ile Leu Asn Ala Gln Thr Val Ser Leu Ser Asn Asp Thr Ile
 405 410 415
 Ala Ile Arg Asp Lys Ala Asp Glu Lys Ile Ile Phe Leu Phe Glu Ala
 420 425 430
 Ser Thr Gly Lys Pro Leu Gly Asp Gly Lys Phe Leu Ser His Lys Asn
 435 440 445
 Glu Ile Leu Glu Ile Ala Leu Asp Gln Lys Gly Leu Thr Asn Asp Arg
 450 455 460
 Lys Ile Ala Phe Ile Asp Lys Asn Arg Asp Leu Cys Ile Thr Ser Val
 465 470 475 480
 Lys Arg Phe Gly Lys Glu Gln Ile Ile Lys Leu Gly Thr Met Val
 485 490 495
 His Thr Leu Ala Trp Asn Asp Thr Cys Asn Ile Leu Cys Gly Leu Gln
 500 505 510
 Asp Thr Arg Phe Ile Val Trp Tyr Tyr Pro Asn Thr Val Tyr Val Asp
 515 520 525
 Arg Asp Ile Leu Pro Lys Thr Leu Tyr Glu Arg Asp Ala Ser Glu Phe
 530 535 540
 Ser Lys Asn Pro His Ile Val Ser Phe Val Gly Asn Gln Val Thr Ile
 545 550 555 560
 Arg Arg Ala Asp Gly Ser Leu Val His Ile Ser Ile Thr Pro Tyr Pro
 565 570 575
 Ala Ile Leu His Glu Tyr Val Ser Ser Lys Trp Glu Asp Ala Val
 580 585 590
 Arg Leu Cys Arg Phe Val Lys Glu Gln Thr Met Trp Ala Cys Leu Ala
 595 600 605
 Ala Met Ala Val Ala Asn Arg Asp Met Thr Thr Ala Glu Ile Ala Tyr
 610 615 620
 Ala Ala Ile Gly Glu Ile Asp Lys Val Gln Tyr Ile Asn Ser Ile Lys
 625 630 635 640
 Asn Leu Pro Ser Lys Glu Ser Lys Met Ala His Ile Leu Leu Phe Ser
 645 650 655
 Gly Asn Ile Gln Glu Ala Glu Ile Val Leu Leu Gln Ala Gly Leu Val
 660 665 670
 Tyr Gln Ala Ile Gln Ile Asn Ile Asn Leu Tyr Asn Trp Glu Arg Ala
 675 680 685
 Leu Glu Leu Ala Val Lys Tyr Lys Thr His Val Asp Thr Val Leu Ala
 690 695 700

Tyr Arg Gln Lys Phe Leu Glu Thr Phe Gly Lys Gln Glu Thr Asn Lys
 705 710 715 720
 Arg Tyr Leu His Tyr Ala Glu Gly Leu Gln Ile Asp Trp Glu Lys Ile
 725 730 735
 Lys Ala Lys Ile Glu Met Glu Ile Thr Lys Glu Arg Glu Gln Ser Ser
 740 745 750
 Ser Ser Gln Ser Ser Lys Ser Ile Gly Leu Lys Pro
 755 760

<210> 42

<211> 760

<212> PRT

<213> Caenorhabditis elegans

<400> 42

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 20 25 30
 Asp Asp His Val Phe Leu Leu Thr Asn Thr Ala Thr Asn Glu Ser Gln
 35 40 45
 Gln Ile Leu Asn Met Pro Glu Thr Phe Phe Pro Thr Ser Leu His Ile
 50 55 60
 Phe Pro Arg Ser Gln Thr Lys Gly Gly Gln Asn Asp Val Phe Ala Val
 65 70 75 80
 Ser Thr Ser Asp Gly Lys Ile Asn Ile Leu Ser Arg Asn Gly Lys Val
 85 90 95
 Glu Asn Met Val Asp Ala His Asn Gly Ala Ala Leu Cys Ala Arg Trp
 100 105 110
 Asn Ser Asp Gly Thr Gly Leu Leu Ser Ser Gly Glu Asp Gly Phe Val
 115 120 125
 Lys Met Trp Ser Arg Ser Gly Met Leu Arg Ser Val Leu Ala Gln Phe
 130 135 140
 Ala Thr Ala Val Tyr Cys Val Ala Trp Asp Ser Thr Ser Ser Asn Val
 145 150 155 160
 Leu Tyr Cys Asn Ala Asp His Cys Tyr Ile Lys Ser Leu Lys Met Gln
 165 170 175
 Val Ala Pro Ile Lys Trp Lys Ala His Asp Gly Ile Ile Leu Cys Cys
 180 185 190
 Asp Trp Asn Pro Thr Ser Asp Leu Ile Val Thr Gly Gly Glu Asp Leu
 195 200 205
 Lys Phe Lys Val Trp Asp Gly Phe Gly Gln Ile Leu Phe Asn Ser Ser
 210 215 220
 Val His Asp Tyr Pro Ile Thr Ser Ile Ser Trp Asn Thr Asp Gly Thr
 225 230 235 240
 Leu Phe Ala Val Gly Ser His Asn Ile Leu Arg Leu Cys Asp Lys Ser
 245 250 255
 Gly Trp Ser His Ser Leu Glu Lys Met Asn Ala Gly Ser Val Met Ala
 260 265 270
 Leu Ser Trp Ser Pro Asp Gly Thr Gln Leu Ala Val Gly Thr Ala Ala
 275 280 285
 Gly Leu Val Phe His Ala His Ile Ile Asp Lys Arg Leu Thr Tyr Glu
 290 295 300
 Glu Phe Glu Ile Val Gln Thr Gln Lys Thr Val Ile Glu Val Arg Asp
 305 310 315 320
 Val Ser Ser Glu Val Ser Arg Glu Thr Leu Glu Thr Lys Glu Arg Ile
 325 330 335

Ser Lys Ile Ala Ile Leu Tyr Lys Tyr Leu Ile Val Val Thr Ser Ser
 340 345 350
 His Ile Tyr Ile Tyr Ser Ser Lys Asn Trp Asn Thr Pro Thr Met Ile
 355 360 365
 Glu Tyr Asn Glu Arg Thr Val Asn Ile Ile Val Gln Cys Glu Lys Ile
 370 375 380
 Phe Leu Val Ser Asp Gly Met Thr Ile Thr Ile Phe Thr Tyr Glu Gly
 385 390 395 400
 Arg Lys Leu Ile Asn Leu Asn Pro Pro Gly Gln Val Met Ala Leu Leu
 405 410 415
 Asp Glu Arg Lys Ile Asp Leu Ala Asn Asp Thr Leu Val Val Arg Asp
 420 425 430
 Arg Ala Asp Asn Lys Val Leu His Phe Phe Asp Pro Thr Thr Gly Lys
 435 440 445
 Ala Gln Gly Asp Gly Asn Leu Lys His Glu His Asp Ile Val Glu Leu
 450 455 460
 Thr Val Asn Gln Cys Gly Pro Leu Asn Asp Arg Asn Val Ala Phe Arg
 465 470 475 480
 Asp Gln Ile Gly Ala Val His Ile Ala Met Val Lys Thr Phe Gly Val
 485 490 495
 Ser Gln Arg Met Val Lys Ile Gly Ser Leu Val Glu Gln Leu Val Phe
 500 505 510
 Asn Asp Val Thr Asn Met Leu Cys Gly Ile Ser Glu Gly Lys Ile Ala
 515 520 525
 Val Trp Pro Leu Pro Asn Val Ala Phe His Asp Arg Asn Leu Leu Gln
 530 535 540
 Lys Ser Leu Ile Gln Lys Asn Ile Gly Ser Val Gly Lys Phe Pro Gln
 545 550 555 560
 Leu Ala Asn Phe Ala Gly Asn Thr Ile Val Ile Arg Lys Ser Asp Gly
 565 570 575
 Cys Leu Leu Pro Thr Gly Ile Leu Pro Phe Tyr Gly Thr Leu Ile Thr
 580 585 590
 Met Ala Ser Gln Ser Lys Trp Asp Gln Ala Ile Arg Leu Cys Arg Ser
 595 600 605
 Ile Gly Asn Asp Thr Met Trp Ala Thr Phe Ala Gly Leu Ala Val Leu
 610 615 620
 His Lys Asn Met Ile Val Met Glu Ile Ala Tyr Ala Ala Leu Glu Asp
 625 630 635 640
 Asp Glu Lys Val Ser Leu Ile Asn Glu Ile Lys Asp Lys Thr Asp Lys
 645 650 655
 Glu Thr Arg Gln Ala Met Gln Val Val Leu Thr Gly Lys Leu Ala Asp
 660 665 670
 Ala Asp Val Leu Leu Glu Arg Ser Gly Leu Ser Phe Arg Ser Leu Met
 675 680 685
 Leu Asn Ile Gln Met Phe Lys Trp Lys Arg Ala Leu Glu Leu Gly Leu
 690 695 700
 Lys Asn Lys Gln Trp Leu Glu Ile Val Met Gly Tyr Arg Glu Lys Tyr
 705 710 715 720
 Leu Lys Asn Cys Gly Gln Lys Glu Thr Asp Pro Leu Phe Leu Lys His
 725 730 735
 Met Ser Glu Val Glu Ile Asp Trp Val His Ile Arg Glu Leu Ile Ala
 740 745 750
 Ala Glu Lys Ala Lys Gly Asn Asn
 755 760

<210> 43

<211> 8

<212> PRT
<213> Chlamydomonas reinhardtii

<400> 43
Leu Glu Gly Glu Thr Asp Gln Ala
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<210> 44
<211> 8
<212> PRT
<213> Chlamydomonas reinhardtii

<400> 44
Gly Ile Asp Pro Tyr Cys Val Glu
1 5

<210> 45
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> primer for PCR

<400> 45
garacbgayc argcbgayaa rta

23

Alf
<210> 46
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> primer for PCR

<400> 46
gcyclvacrc artavgggrtc rat

23

<210> 47
<211> 27
<212> PRT
<213> Chlamydomonas reinhardtii

<400> 47
Ala Ala Thr Asn Leu Ala Phe Leu Tyr Phe Leu Glu Gly Glu Thr Asp
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Gln Ala Asp Lys Tyr Ser Glu Met Ala Leu Lys
20 25

<210> 48
<211> 26
<212> PRT
<213> Chlamydomonas reinhardtii

<400> 48
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1 5 10 15

Ile Tyr Asn Leu Gly Leu Val Ser Gln Arg
20 25

<210> 49
<211> 11
<212> PRT
<213> Chlamydomonas reinhardtii

<400> 49
Gly Val Tyr Phe Asp Glu Asp Phe His Val Arg
1 5 10

<210> 50
<211> 11
<212> PRT
<213> Chlamydomonas reinhardtii

<400> 50
Tyr Val Ser Ala Ile Asp Gln Gln Val Glu Arg
1 5 10

AP